

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 30, 2002, 14:59:19 : Search time 41.9 Seconds

(without alignments)  
3719.249 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 7308

Sequence: 1 MATQKASDRISQFDHNL.....SKYLIQKWLPSPIQK 1403

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A-Geneseq.032802:\*

1:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7308	100.0	1403	18 AAM20032	Neuronal apoptosis
2	7308	100.0	1403	20 AAY14079	Gonadotrophic hormo
3	7308	100.0	1403	21 AAY09539	Human apoptosis in
4	7308	100.0	1403	21 AAY09539	Human NAIP protein
5	7284	99.7	1403	18 AAM20033	Neuronal apoptosis
6	6691	91.6	1295	20 AAY14080	Gonadotrophic hormo
7	6691	91.6	1295	20 AAY09540	Human apoptosis in
8	6373.5	87.2	1332	17 AAR98217	Human apoptosis in
9	661	9.0	1204	22 AAU02881	Human caspase recr
10	654	8.9	1070	22 AAG67527	Amino acid sequenc
11	653	8.9	1024	22 AAU02880	Human caspase recr

12	566	7.7	841	22 AAM23595	Murine EST encoded
13	545.5	7.5	118	21 AAB53493	Human colon cancer
14	536.5	7.3	738	22 AAG67526	Amino acid sequenc
15	462	6.3	618	18 AAM19746	Human inhibitor of
16	462	6.3	618	18 AAM19583	Human apoptosis in
17	462	6.3	618	18 AAM13545	Human c-IAP1. Hom
18	462	6.3	618	19 AAM69296	Human H1AP-2 prote
19	462	6.3	618	20 AAY33998	Human cellular inh
20	457.5	6.3	612	18 AAM13555	Murine c-IAP. Mus
21	457.5	6.3	612	19 AAM69299	Murine H1AP-2 prot
22	441.5	6.0	591	18 AAM19586	Mouse apoptosis in
23	440	6.0	600	19 AAM69298	Murine H1AP-1 prot
24	437.5	6.0	496	18 AAM19584	Mouse apoptosis in
25	437.5	6.0	496	19 AAM69297	Murine XIAP protei
26	436.5	6.0	604	18 AAM19747	Human inhibitor of
27	436.5	6.0	604	18 AAM13546	Human c-IAP2. Hom
28	436.5	6.0	604	20 AAY52703	Human cellular inh
29	436.5	6.0	604	20 AAY33997	Human cellular inh
30	435	6.0	1141	22 AAB50694	Human APT2-MUT chl
31	431.5	5.9	496	18 AAM19745	Mouse inhibitor of
32	431.5	5.9	604	18 AAM19582	Human apoptosis in
33	431.5	5.9	604	19 AAM69295	Human H1AP-1 prote
34	427.5	5.8	602	18 AAM19585	Mouse apoptosis in
35	407	5.6	497	21 AAY59451	Human XIAP protein
36	403	5.5	497	18 AAM19581	Human apoptosis in
37	403	5.5	497	19 AAM69294	Human XIAP protein
38	403	5.5	497	21 AAY99985	Human X-Linked inh
39	354	4.8	642	22 AAM25640	Human protein sequ
40	340.5	4.7	438	17 AAM04583	Human inhibitor of
41	336	4.6	498	22 ABB62863	Drosophila melanog
42	335	4.6	498	18 AAM19748	Human secreted pro
43	320	4.4	60	21 AAG01849	Angiotensin conver
44	318.5	4.4	306	22 AAU02925	Human
45	304.5	4.2	438	22 AAB48191	Drosophila mutant

#### ALIGNMENTS

RESULT 1					
AAM20032					
ID	AAM20032 standard; Protein; 1403 AA.				
XX					
XX	AAM20032:				
XX					
XX	06-OCT-1997 (first entry)				
XX					
XX	Neuronal apoptosis inhibitor protein (NAIP).				
DE					
XX					
KW	Neuronal apoptosis inhibitor protein; NAIP; diagnosis;				
KW	therapy; cancer; AIDS; amyotrophic lateral sclerosis;				
KW	spinal muscular atrophy.				
XX					
OS	Homo sapiens.				
XX					
PN	W09726331-A2.				
XX					
PD	24-JUL-1997.				
XX					
PI	17-JAN-1997; 57MO-IB00142.				
XX					
PF	19-JAN-1996; 96GB-0001108.				
XX					
PR	(UYOT-) UNTV OTTAWA.				
XX					
PA	Korreluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K;				
XX					
PI	WPI: 1997-38535/35.				
XX					
DR	N-PSDB: AAT71265.				
XX					
PT	New neuronal inhibitor of apoptosis - useful for diagnosing and				
XX	treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis				

PS Claim 41: Fig 6A-I; 102pp; English.

XX Novel human neuronal apoptosis inhibitor protein (AAW20032), or NAIP,  
CC is a negative regulator of apoptosis, partic. neuronal apoptosis  
CC and, when deficient or absent, contributes to neurodegenerative  
CC phenotypes such as spinal muscular atrophy (SMA) and amyotrophic  
CC lateral sclerosis. Its amino acid sequence was deduced from a  
CC cDNA clone (AA771265) obt. from a human foetal spinal cord cDNA  
CC library. NAIP polypeptides, esp. those containing at least two  
CC BIR (baculovirus IAP repeat) domains, can be expressed in host  
CC vector systems and used to increase or induce apoptosis in host  
CC treatment of AIDS, neurodegenerative disease, amyloidopathic  
CC syndromes or ischemic injury, to screen for (anti)agonists, or to  
CC produce antibodies useful for inhibiting apoptosis.

Sequence 1403 AA:

Query Match 100.0%; Score 7308; DB 18; Length 1403;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MATQKASDERISOFDNLPELSALIGDAVQALKEEEROKRAMQGYNSMRSE 60  
1 mactqksderisqfndhlpelsaligdayqlakeleeeqetramqgyngmrse 60  
61 AKRLKFTVTEPYSSWIPOEMAAGFYFGVSGIQCCSLIFGAGLRPLPEDIHRRF 120  
61 akrlkftvtepysswipemaaagfytgysgicccslifgaglrplpeditrrf 120  
121 HPDCGLLKKDYNIAKYDIRYKLNKSLRGKMKRYDEEARLASFFNMFFYQGISPCV 180  
121 hpdcgllkkdyngiakydrryknksrlrgkmrydeearlasffnmffyqgispcv 180  
181 LSEAGVFNGKDYQVQCCSCGCGGNNWEGDDPKWEHAKWPCFELRKKSSSEETQYI 240  
181 lseagvfngkdyvqccscgcggnnwegddpkwehkwpcfelrkkssseetqyi 240  
241 OSYKGFVDITGEHFVNSVWQRELPMASAYCNDISFAYEELRLDSFKNMREAVAVALA 300  
241 osykgfvditgehfvnswqrelpmasaycndisfayeelrldsfknmreavavala 300  
301 KAGFYGINDIYQCFSCGCGCLEKWOEGDDPLDDHTRCPNCPNCPNCPNCPNCPNCPN 360  
301 kagfygindiyqcfscgcgclekwoegddplddhtrcpncpncpncpncpncpn 360  
361 RGELECELETTSESNEEDSIAGPIVPEMAOCEAOMFODAKNLEOLRAAYTSAPFRHMS 420  
361 rgeleceleTTSESNEEDSIAGPIVPEMAOCEAOMFODAKNLEOLRAAYTSAPFRHMS 420  
421 LLDISSDLATDHLGCDLSIAKSHISKVQVPLVPEVFGNLNSVMVEGEAGSGTVLL 480  
421 lldissdlatdhlgcdlsiakshiskvqvpplvpevfgnlnsvmvegeagsgtvll 480  
481 KKIAPLMAAGCCPLLNRFQVLYSLSTRPDEGLASITDOLLEKSGVTECKMNIITQ 540  
481 kkiaplmaagccpllnrfqvlyslstrpdeglasitdolleksgvteckmniitq 540  
541 OKKNQVLEFLDDYKICISIPVIGIKLOKHNLSRTCLLAVFTNRARDRLRETLITLITK 600  
541 okknqvleflddykicisipvigiklokhnlstrcllavftnrardrlretilitk 600  
601 APEFYNTVCIRKLFSNNMTRLRKFWYFGKNOSLOKIOKTLFLFAALCAHMFQYEDPS 660  
601 apefyntvcirklfsnnmtrlrkfwyfgknoslokioktlflfaalhmfqyedps 660  
661 FDDVAVFYSYMERLSLNKATAILKATYSGCCGLALGFSSCCGFDDDLAAGVDED 720  
661 fddvavfysymerlslnkatailkatysgccglalgfssccgfdddlagvded 720  
721 EDLTMCLMSFTAQRLRPYREFLSAPQFELAGMLRLILSDSQEHOQDGLYHLQINS 780  
721 edltmlcmstfaqrlrpyreflsapqfelagmlrlilsdsqehoqdglyhlqins 780

QY 781 PMATVSAVNNFLNVSSSLPSTKAGPKIVSHLLHLVDNKNESLENISENDYLRKHQPEISLO 840  
DB 781 pmatvsavnnflnvssslpstkagpkivshllhlvdnkneselelendylyrkhppeislo 840  
QY 841 MOLLRGMOICPQAVRSNMSSEHLVALKTAQVSNNTVAAGSPFLQFLOCRITLTLGALNT 900  
DB 841 mollrgmoicpqavrsnmssehlvalktaqvsnntvaagspflqflocritltlgaln 900  
QY 901 QYFDDPESLSLRISHPIRGNKTSPPRAHSVLETGCRDSQVFFTDQVAFEPENEM 960  
DB 901 qyfdpeslslrishpirgnktspprahsvletgcrdsqvfftdqvafepenem 960  
QY 961 ERNLEKEEDNYSYMDNRASPLSTGYWKLSPKQYKIRPLEVDVNDIDVYQOMLETL 1020  
DB 961 ernlekeednysymdnrasplstgywklspkqykirplevdvndidvyqomletl 1020  
QY 1021 MTFVSASQRIELHNSRGFTESIRPALERISKASYKCSIKLELSAAEQELTLPLSE 1080  
DB 1021 mtfvsasqrielhnsrgftesirpaleriskasykcsiklelsaaeqeltlplse 1080  
QY 1081 SLEVSCTIOSODIFPMLDKETLKLSTVDEGNINVSVPJPEEPNPHHEKILLIOISA 1140  
DB 1081 slevsctiosodifpmldketlklstvdegninvsvpjpeepnphhekillioisa 1140  
QY 1141 EYDPSKLVKLIQNSPULHYPHLKCNFSDGSLMTLVSCKKLEIRFSDSFGQAVFVA 1200  
DB 1141 eydpskvlvqliqnsplhphlkcndfsgslmtlvscckleirfsgdsgqavfva 1200  
QY 1201 SLNFTISLILNLEGOQPEDETSKFAVITIGSLNSLELTIPRGDITRYAAKLIIOQCO 1260  
DB 1201 slnftislilnlegoqpeдетskfavitigslnsleltiprgditryaakliioqco 1260  
QY 1261 QJHCLRVLSFFKTLNDDSVELAKVAISGQKLENLKLSINRKITEEGYRNFQALDNM 1320  
DB 1261 qjhcrlvlsffktlnddsvelakvaisgqklenlklsinrkiteegyrfnfqaldnm 1320  
QY 1321 PNLGELDLSRFTETECIAQOATVYKLSQCVLRPLRLRLMMLSLMLDADIALVMKMR 1380  
DB 1321 pnlgeldlsrfteteciaqoatvyklsqcvlrplrlrlmmlslmldadialvmkmer 1380  
QY 1381 HPQSKYLTLLQKWLIPSPPIIOK 1403  
DB 1381 hpqskyltllqkwllpspiioK 1403

RESULT 2  
AAV14079  
ID AAV14079 standard; Protein: 1403 AA.  
AC AAV14079;  
DT 20-JUL-1999 (first entry)  
DE Gonadotropic hormone protein sequence.  
KW Gonadotropic hormone: excessive ovulation animal; transgenic animal;  
KW totipotent cell; somatic cell chromosome.  
OS Homo sapiens.  
PN JPI1113444-A.  
PD 27-APR-1999.  
PF 14-OCT-1997; 97JP-0280830.  
PR 14-OCT-1997; 97JP-0280830.  
PX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
PY (SAKA/) SAKAI H.  
XX WPI: 1999-320709/27.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 30, 2002, 15:03:59 : Search time 16.67 Seconds  
(without alignments)  
3258.760 Million cell updates/sec

Title: US-09-830-338-1  
Perfect score: 7308  
Sequence: 1 MATQKASDERISQPDHNL.....SKYTLQKWLPEFSPITCK 1403

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7308	100.0	1403	B1R1_HUMAN	Q13075 homo sapien
2	4956	67.8	1403	B1R1_MOUSE	Q9gwk3 mus musculu
3	4919	67.3	1447	B1R1_MOUSE	Q9guk4 mus musculu
4	4885	66.8	1403	B1R1_MOUSE	Q91016 mus musculu
5	4811	65.8	1403	B1R1_MOUSE	Q911b6 mus musculu
6	4796.5	65.6	1402	B1R1_MOUSE	Q911b3 mus musculu
7	654	8.9	1024	B1R1_MOUSE	Q911p4 mus musculu
8	462	6.3	612	B1R1_MOUSE	Q13490 homo sapien
9	457.5	6.3	612	B1R1_MOUSE	Q62210 mus musculu
10	440	6.0	600	B1R1_MOUSE	Q08863 mus musculu
11	436.5	6.0	604	B1R1_MOUSE	Q13489 homo sapien
12	431.5	5.9	496	B1R1_MOUSE	Q60989 mus musculu
13	416.5	5.7	496	B1R1_MOUSE	Q91016 mus musculu
14	407	5.6	497	B1R1_MOUSE	Q91016 mus musculu
15	388	5.3	611	B1R1_MOUSE	Q91016 mus musculu
16	385	4.6	498	B1R1_MOUSE	Q91016 mus musculu
17	326	4.5	358	B1R1_MOUSE	Q91016 mus musculu
18	303.5	4.2	275	B1R1_MOUSE	Q91016 mus musculu
19	301	4.1	438	B1R1_MOUSE	Q91016 mus musculu
20	293.5	4.0	268	B1R1_MOUSE	Q91016 mus musculu
21	201.5	2.8	1062	B1R1_MOUSE	Q91016 mus musculu
22	198	2.7	1473	B1R1_MOUSE	Q91016 mus musculu
23	194.5	2.7	997	B1R1_MOUSE	Q91016 mus musculu
24	192	2.6	1453	B1R1_MOUSE	Q91016 mus musculu
25	182	2.5	953	B1R1_MOUSE	Q91016 mus musculu
26	180.5	2.5	3210	B1R1_MOUSE	Q91016 mus musculu
27	175.5	2.4	275	B1R1_MOUSE	Q91016 mus musculu
28	167	2.3	4540	B1R1_MOUSE	Q91016 mus musculu
29	166.5	2.3	1040	B1R1_MOUSE	Q91016 mus musculu
30	165.5	2.3	1315	B1R1_MOUSE	Q91016 mus musculu
31	164.5	2.3	286	B1R1_MOUSE	Q91016 mus musculu
32	163	2.2	239	B1R1_MOUSE	Q91016 mus musculu
33	163	2.2	1041	B1R1_MOUSE	Q91016 mus musculu

## ALIGNMENTS

RESULT 1  
B1R1\_HUMAN STANDARD: PRT: 1403 AA.  
AC Q13075: Q13730: Q99196: Q75857:  
BT 01-NOV-1997 (Rel. 35, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 1 (neuronal apoptosis  
inhibitory protein).  
GN BIR1 OR NAIP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=95112344; PubMed=7813013;  
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraqhi Z.,  
RA Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,  
RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,  
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;  
RT "The gene for neuronal apoptosis inhibitory protein is partially  
deleted in individuals with spinal muscular atrophy.";  
RL Cell 80:167-178(1995).  
[2]  
RP SEQUENCE FROM N.A., AND REVISIONS.  
RC TISSUE=Brain;  
RX MEDLINE=96163755; PubMed=9503025;  
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,  
RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,  
RA Mackenzie A.E.;  
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular  
atrophy candidate genes SMN and NAIP.";  
RL Genomics 48:121-127(1998).  
[3]  
RP SEQUENCE OF 386-623 FROM N.A.  
RC der Steege G., Draalijers T.G., Grootscholten P.M., Olinga J.,  
RA Anzelino R., Vellona I., Brahe C., Scheffer H., van Ommen G.J.B.,  
RA Buys C.H.C.M.;  
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
RL [4]  
RP SEQUENCE OF 222-1403 FROM N.A.  
RC Jones K., Graves T., McPherson J.;  
RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RL [5]  
RP FUNCTION.  
RC TISSUE=Liver;  
RX MEDLINE=96149249; PubMed=9552191;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
family of IAP genes.";  
RL Nature 379:349-353(1996).  
CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSOR  
 CC NEURONS. FOUND IN LAYER AND PLACENTA, AND IN A LESSER EXTENT IN  
 CC SPINAL CORD.  
 CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN  
 CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS  
 CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I  
 CC (WERNICKE-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE  
 CC III (WOLFF-PARK-KUDELBERG-WELANDER DISEASE) BASED UPON THE AGE OF  
 CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE  
 CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO  
 CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000  
 CC MEMBERS.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC DR EMBL: U19251; AAC52045.1; -  
 CC DR EMBL: U80017; AAC52047.1; -  
 CC DR EMBL: U21913; AAA64504.1; -  
 CC DR EMBL: AC005031; AAC62261.1; -  
 CC DR HSBP: Q13490; IQBH.  
 CC DR MIM: 600355; -  
 CC DR InterPro: IPR001370; BIR.  
 CC DR Pfam: PF00653; BIR; 3.  
 CC DR SMART: SM00238; BIR; 3.  
 CC DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 CC DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 CC DR PROSITE: PS50837; NACHT; 1.  
 CC KM Apoptosis; Repeat.  
 CC FT REPEAT 60 127 BIR 1.  
 CC FT REPEAT 159 227 BIR 2.  
 CC FT REPEAT 278 345 BIR 3.  
 CC FT DOMAIN 464 758 NACHT.  
 CC FT CONFLICT 222 223 PK -> YR (IN REF. 4).  
 CC FT CONFLICT 386 387 VP -> ST (IN REF. 3).  
 CC FT CONFLICT 535 535 Y -> V (IN REF. 3).  
 CC FT CONFLICT 553 553 Y -> H (IN REF. 3).  
 CC FT CONFLICT 1228 1231 MISSING (IN REF. 4).  
 CC SQ SEQUENCE 1403 AA: 159613 MW: 566304C134DA5E64 CRC64;  
 CC  
 CC Query Match 100.0% Score 7308; DB 1; Length 1403;  
 CC Best Local Similarity 100.0% Pred. No. 0;  
 CC Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 KAGLFYTGDKIDVOCFSCGGCLEKWEQGDPLDHTRCFPCFPLQNMKMSAEVTPDDLS 360  
 OY 361 RELCELETTSESNELEDSIAVPTPEMAQGEAOMPOKAKNLEOLRAAYTSASFRHS 420  
 Db 361 RELCELETTSESNELEDSIAVPTPEMAQGEAOMPOKAKNLEOLRAAYTSASFRHS 420  
 OY 421 LLDISSDLATHLGCDDLSIAKHSKIPVDEPLVPEVGNLSVNCVGEAGSGKTVLL 480  
 Db 421 LLDISSDLATHLGCDDLSIAKHSKIPVDEPLVPEVGNLSVNCVGEAGSGKTVLL 480  
 OY 481 KKIPIAASGCCPLANRPOLVPLSLSTPRDEGLASIIICDOLKESSVTEMKRNIIQ 540  
 Db 481 KKIPIAASGCCPLANRPOLVPLSLSTPRDEGLASIIICDOLKESSVTEMKRNIIQ 540  
 OY 541 QLNQOVFLLDYKEICISIPQVIGKLIQKNHSRCLLAIVTNRNARDIRRYLETILEIK 600  
 Db 541 QLNQOVFLLDYKEICISIPQVIGKLIQKNHSRCLLAIVTNRNARDIRRYLETILEIK 600  
 OY 601 AFPEYNTVCLIRKLFESHNTRLKRENVYFGKNQSLQIKTPLEFYAAICAHMPQPPDPS 660  
 Db 601 AFPEYNTVCLIRKLFESHNTRLKRENVYFGKNQSLQIKTPLEFYAAICAHMPQPPDPS 660  
 OY 661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELATKGFFSCCFEPNDDLAEGVDED 720  
 Db 661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELATKGFFSCCFEPNDDLAEGVDED 720  
 OY 721 EDLTMCIMSKFTAOBLRPFRPLSLPAFOELAGNRLIELDSDROEHQDGLHLMQINS 780  
 Db 721 EDLTMCIMSKFTAOBLRPFRPLSLPAFOELAGNRLIELDSDROEHQDGLHLMQINS 780  
 OY 781 PMMTVSAINNPLNVVSSLPSTKAGPKIYSHLLHYDKESLENISENDYLYKHQPEISLQ 840  
 Db 781 PMMTVSAINNPLNVVSSLPSTKAGPKIYSHLLHYDKESLENISENDYLYKHQPEISLQ 840  
 OY 841 MOLLRLGMOICPOAVFMSVSEHLVYLAKTAYQSNVVAACSPVLOFLGRTLTGALNL 900  
 Db 841 MOLLRLGMOICPOAVFMSVSEHLVYLAKTAYQSNVVAACSPVLOFLGRTLTGALNL 900  
 OY 901 QYFDPHDESLSLRSIHPIRGNKTSBRAHFSVLETCFDPKSOVPTIDDDYASAFENNEW 960  
 Db 901 QYFDPHDESLSLRSIHPIRGNKTSBRAHFSVLETCFDPKSOVPTIDDDYASAFENNEW 960  
 OY 961 ERNLAEKEDNVKSYMOMORASPDLSGTWKLSPYOYKIPCLEVDVNDIDVVGQDMLEIL 1020  
 Db 961 ERNLAEKEDNVKSYMOMORASPDLSGTWKLSPYOYKIPCLEVDVNDIDVVGQDMLEIL 1020  
 OY 1021 MTFVSASORTELHANSRGFTESIRPALELSKASVTKCSISKLELSAAEOBELTLTPSLE 1080  
 Db 1021 MTFVSASORTELHANSRGFTESIRPALELSKASVTKCSISKLELSAAEOBELTLTPSLE 1080  
 OY 1081 SLEVSQTIQSOQIIPNLDKFLCLKELSVLDLGNINPFSVYPRDEFPMHMEKLLQISA 1140  
 Db 1081 SLEVSQTIQSOQIIPNLDKFLCLKELSVLDLGNINPFSVYPRDEFPMHMEKLLQISA 1140  
 OY 1141 EYDPSKIVLYLQNSNLVAFHLKCNFSDFOSLMTMLVSCKLTLETIKFSDFQOAPFVA 1200  
 Db 1141 EYDPSKIVLYLQNSNLVAFHLKCNFSDFOSLMTMLVSCKLTLETIKFSDFQOAPFVA 1200  
 OY 1201 SLNPFISLKIILNLEGOQFPDEETSEKFAVILGSLSNLEBELPTFGDGIYRAVKLLIQCO 1260  
 Db 1201 SLNPFISLKIILNLEGOQFPDEETSEKFAVILGSLSNLEBELPTFGDGIYRAVKLLIQCO 1260  
 OY 1261 OLHCRLVLSFPKTLNDSSVEIAKVALISGGFQKLEMLKISINHKTITEERYRNFQALDNM 1320  
 Db 1261 OLHCRLVLSFPKTLNDSSVEIAKVALISGGFQKLEMLKISINHKTITEERYRNFQALDNM 1320  
 OY 1321 PNLQELDISRHFTCEICIAQATYKSLSCCVLRLPRLIRLNLMSWLLDADIALNVYKER 1380  
 Db 1321 PNLQELDISRHFTCEICIAQATYKSLSCCVLRLPRLIRLNLMSWLLDADIALNVYKER 1380  
 OY 1381 HPQSKYITLQKLTLPSPQIOLK 1403

Db 1381 HPOSXYTLILQKMLPSPFIQK 1403

## RESULT 2

BIRL\_MOUSE STANDARD: PRT: 1403 AA.

AC 09QK5: 09R017: 09JIB5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis inhibitory protein 1).

GN BIRCL1 OR NAIP1 OR NAIP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RA Yaraqul Z., Korneluk R.G., Mackenzie A.E.;

RT "Cloning and characterization of the multiple copies of the murine homologue of NAIP (neuronal apoptosis inhibitory protein).";

RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.

RN (2)

RP SEQUENCE FROM N.A.

RA MEDLINE-99431676; PubMed-10501978;

RT Huang S., Scharf J.M., Gowney J.D., Endrizzi M.G., Dietrich W.F.;

RL "The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts.";

RL Mamm. Genome 10:1032-1035(1999).

RN (3)

RP SEQUENCE FROM N.A.

RA MEDLINE-20414747; PubMed-10958627;

RT Endrizzi M.G., Hadinoto V., Gowney J.D., Miller W., Dietrich W.F.;

RL "Genomic sequence analysis of the mouse Naip gene array.";

CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.

CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.

CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.

CC -----

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CC -----

DR EMBL: AF007769; AAB69223.1; -

DR EMBL: AF135491; AAD56763.1; -

DR EMBL: AF242432; AAF82752.1; -

DR HSSP: Q13490; IQBH.

DR MGD: MGI:1298223; Birc1a.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR: 3

DR SMART: SM00238; BIR: 3

DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.

DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.

DR PROSITE: PS0837; NACHT; 1.

DR Apoptosis; Repeat; Multigene family.

FT REPEAT 60 127 BIR 1.

FT REPEAT 159 227 BIR 2.

FT REPEAT 278 345 BIR 3.

FT DOMAIN 464 758 NACHT.

FT EMBL 343 343 I -> V (IN REF. 2).

FT CONFLICT 359 359 L -> Q (IN REF. 2).

FT CONFLICT 624 624 E -> K (IN REF. 2).

FT CONFLICT 1092 1092 D -> E (IN REF. 3).

FT CONFLICT 1116 1116 D -> N (IN REF. 3).

FT CONFLICT 1123 1123 G -> R (IN REF. 3).

FT CONFLICT 1129 1129 L -> H (IN REF. 1).

FT CONFLICT 1140 1140 T -> M (IN REF. 2).

FT CONFLICT 1269 1269 A -> V (IN REF. 3).

SEQ SEQUENCE 1403 AA: 158692 MW: B31630259595EE67 CRC64:

Query Match 67.8%; Score 4956; DB 1; Length 1403;

Best Local Similarity 68.4%; Pred. No. 2,7e-266;

Matches 958; Conservative 158; Mismatches 285; Indels 0; Gaps 0;

QY 1 MATQKASDERISQDHLNLPGLSLDLVQLAKLEEEBQKRAKMGKYSQMSQ 60

DB 1 MAHEGSESDRISEIDYFELPGLSLGVDAVOLAKSOEEBHKRMKMGKFSQMS 60

QY 61 AKRLTFVTEYEPYSWIRQEMAAAGFYTGKSGIOCCSILIFGALITRLPTDHRF 120

DB 61 AKRLTFEETYPDFRKTWTQEMAAAGFYTGKSGIOCCSILIFGALITRLPTDHRF 120

QY 121 HPDCGFLLNKDVGNIAKYDIRKNLSRLRGKMRVQEEEARLASFRMPPYVQISPCV 180

DB 121 RPECFLQGDVGNIGKIDYRKSPKMLRGKARYHEEARLESFEDMPPYVQISPCV 180

QY 181 LSEAGFVTTGKQDYQVQCFSCGCGCLGNWEGDDPMKEHAKMKPKCFGLSKSSSEITQYI 240

DB 181 LSAAGFVTTGKRDYQVQCFSCGCGSLGNWEGDDPMKEHAKMKPKCFGLSKSSSEITQYI 240

QY 241 OSYKGFVDITGEHFVNSWVQRELPMASAYCNDISIFAYEELRLDSFRKDPRESAVGVALA 300

DB 241 OYEGSFVHTGHEFVNSWVQRELPMASAYCNDISIFAYEELRLDSFRKDPRESAVGVALA 300

QY 301 KAGLFYTGIRKIDYQVQCFSCGCGCLEKMQEGDDPLDHTRCFPNCPFLQNNKSSAENVTPDLOS 360

DB 301 KAGLFYTGIRKIDYQVQCFSCGCGCLEKMQEGDDPLDHTRCFPNCPFLQNNKSSAENVTPDLOS 360

QY 361 RAGLFYTGIRKIDYQVQCFSCGCGCLEKMQEGDDPLDHTRCFPNCPFLQNNKSSAENVTPDLOS 360

DB 361 RAGLFYTGIRKIDYQVQCFSCGCGCLEKMQEGDDPLDHTRCFPNCPFLQNNKSSAENVTPDLOS 360

QY 420 RGLCELLLETTSESLSLQESIAVGPVPEMAQCEAQMPOBAKLNQPLAATTSASFRMS 420

DB 420 RGLCELLLETTSESLSLQESIAVGPVPEMAQCEAQMPOBAKLNQPLAATTSASFRMS 420

QY 421 HCALEPAMETTESNSHDDPAVAHSTVGLGREAQWFOEARSLSQLDNDNTKATFRHNN 420

DB 421 HCALEPAMETTESNSHDDPAVAHSTVGLGREAQWFOEARSLSQLDNDNTKATFRHNN 420

QY 480 LLDISSDLATDHLACDLSIASKHSIKPQOEVLPEVFGNLSVQCEGASCKTYVL 480

DB 480 LLDISSDLATDHLACDLSIASKHSIKPQOEVLPEVFGNLSVQCEGASCKTYVL 480

QY 481 KRIAFMASGCCPPLNRFQVLYSLSTRDEGLASITICDQLKEGCVTEMCRNITQ 540

DB 481 KRIAFMASGCCPPLNRFQVLYSLSTRDEGLASITICDQLKEGCVTEMCRNITQ 540

QY 540 KRIAFMASGCCPPLNRFQVLYSLSTRDEGLASITICDQLKEGCVTEMCRNITQ 540

DB 540 KRIAFMASGCCPPLNRFQVLYSLSTRDEGLASITICDQLKEGCVTEMCRNITQ 540

QY 541 QLNQVLELDDYKKEICISPOYIGKLIQKNHSRCLIAVNTNARIDIRLETILEIK 600

DB 541 QLNQVLELDDYKKEICISPOYIGKLIQKNHSRCLIAVNTNARIDIRLETILEIK 600

QY 600 QLNQVLELDDYKKEICISPOYIGKLIQKNHSRCLIAVNTNARIDIRLETILEIK 600

DB 600 QLNQVLELDDYKKEICISPOYIGKLIQKNHSRCLIAVNTNARIDIRLETILEIK 600

QY 660 AEPFYNTVCILRKLSHMTRLRKPMVYFGKQKSLQKIOKPLVPAALCAHMFQVPPFPS 660

DB 660 AEPFYNTVCILRKLSHMTRLRKPMVYFGKQKSLQKIOKPLVPAALCAHMFQVPPFPS 660

QY 661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELALGFTSCCFEFDNDLAEAGVED 720

DB 661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELALGFTSCCFEFDNDLAEAGVED 720

QY 720 FQDMALFVSQYQVLSLKKGAQAKPLQATVSSCGELALGFTSCCFEFDNDLAEAGVED 720

DB 720 FQDMALFVSQYQVLSLKKGAQAKPLQATVSSCGELALGFTSCCFEFDNDLAEAGVED 720

QY 721 EDLIMCLMSKFTAOQLRPYRFLSPAFQELAGMLIELSDROHDLGLYHLQINS 780

DB 721 EDLIMCLMSKFTAOQLRPYRFLSPAFQELAGMLIELSDROHDLGLYHLQINS 780

QY 780 EDLIMCLMSKFTAOQLRPYRFLSPAFQELAGMLIELSDROHDLGLYHLQINS 780

DB 780 EDLIMCLMSKFTAOQLRPYRFLSPAFQELAGMLIELSDROHDLGLYHLQINS 780

QY 840 PMMTVASANNPLNPLVSSLPSTKAGKIVSHLHLVDNKESENISENDYGLKHOEISLQ 840

DB 840 PMMTVASANNPLNPLVSSLPSTKAGKIVSHLHLVDNKESENISENDYGLKHOEISLQ 840

QY 841 PLKALTITNNPLKIVFSHPSSKAGPLVSHLHLVDNKESENISENDYGLKHOEISLQ 840

DB 841 PLKALTITNNPLKIVFSHPSSKAGPLVSHLHLVDNKESENISENDYGLKHOEISLQ 840

QY 841 MOLNGLMOICPOAFVSWSEHLVLAALKTAVOSNTVACSFVLOFLQRTLTGALNL 900

DB 841 MOLNGLMOICPOAFVSWSEHLVLAALKTAVOSNTVACSFVLOFLQRTLTGALNL 900

QY 900 MKGLKELMILSPREYSSVSEHLRLALNPAVESVTAECSPFIQPLRGRTLAKVNL 900

DB 900 MKGLKELMILSPREYSSVSEHLRLALNPAVESVTAECSPFIQPLRGRTLAKVNL 900

QY 901 QYFQHPESLSLSLRNTHIRPKNTSPRAHFSVLETCGDKSOVPTIDYVSAFEPANW 960

DB 901 QYFQHPESLSLSLRNTHIRPKNTSPRAHFSVLETCGDKSOVPTIDYVSAFEPANW 960

QY 960 QYFRDHPESLSLSLRNTHIRPKNTSPRAHFSVLETCGDKSOVPTIDYVSAFEPANW 960

DB 960 QYFRDHPESLSLSLRNTHIRPKNTSPRAHFSVLETCGDKSOVPTIDYVSAFEPANW 960

QY 961 ENRLAEKEDNVKSYNDMDQRRASPDLSGTGYWKLSPQYRIPLCELVYDNDIDVVGDMLEIL 1020

DB 961 ENRLAEKEDNVKSYNDMDQRRASPDLSGTGYWKLSPQYRIPLCELVYDNDIDVVGDMLEIL 1020

```

Db 961 EKNLSSENEETIKSIKNIIFLOPPKISSGIMKLSRCKIPRLKLEGVNMGPAQALLOVL
OY 1021 MTFVFSASQRIEHLNHSRGLIESIRPALELSKASVTCISKISLESAQDELLTTPSIE
Db 1021 MEVFSASQRIEHLNHSRGLIESIRPALELSKASVTCISKISLESAQDELLTTPSIE
OY 1081 SLEVGSTIQSDQIFPNIDKFLCKELSVDEGINVFSVPEEPFNHMEKLLIQISA
Db 1081 SLEVGSTIQSDQIFPNIDKFLCKELSVDEGINVFSVPEEPFNHMEKLLIQISA
OY 1141 EYDPSKLVKLIONSPNHLVHFLKCNFSDGSLMTLVSCKLTFTKFSDFEQAVPRYA
Db 1141 EYDPSKLVKLIONSPNHLVHFLKCNFSDGSLMTLVSCKLTFTKFSDFEQAVPRYA
OY 1201 SLPEFISLKLINLEGOQFDEETSEKFAVILGSLNLELILPFGDGIYRAKLIIQCCQ
Db 1201 SLPEFISLKLINLEGOQFDEETSEKFAVILGSLNLELILPFGDGIYRAKLIIQCCQ
OY 1261 QLHCLRVLSFFFTLNDSDVVEIAKVAISGQFQKLENLKLSINRKTTEGGRNFPQALDNL
Db 1261 QLHCLRVLSFFFTLNDSDVVEIAKVAISGQFQKLENLKLSINRKTTEGGRNFPQALDNL
OY 1321 PNLOEIDISRHFTBECIKAOATTVKSLSCQVLRPLRLIAMLNMLDADIDALLNPKER
Db 1321 PNLOEIDISRHFTBECIKAOATTVKSLSCQVLRPLRLIAMLNMLDADIDALLNPKER
OY 1381 HQSKYTLTILOKWILFSPPII 1401
Db 1381 HQSKYTLTILOKWILFSPPII 1401
OY 1381 HPOSKRLIIFMKWIVFSPV 1401
Db 1381 HPOSKRLIIFMKWIVFSPV 1401

RESULT 3
BIRB_MOUSE STANDARD: PRT: 1447 AA.
AC 090UK4: 09R030: 009124;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1b (Neuronal apoptosis
inhibitory protein 2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN 11
RP SEQUENCE FROM N.A.
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Nalp gene cluster on Chromosome 13 encodes several distinct
functional transcripts."
RL Mamm. Genome 10:1032-1035(1999).
RN 12
RP SEQUENCE FROM N.A.
RA Yaregali Z., Dietz E., Gros P., Mackenzie A.;
RT "cDNA cloning and the 5' genomic organization of Nalp2, a candidate
gene for murine Legionella resistance."
RL Mamm. Genome 10:761-763(1999).
RN 13
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV:
RA Endrizzi M., Huang S., Scharf J.M., Ketter A.R., Wirth B.,
RT "Comparative sequence analysis of the mouse and human Lgn1/SMA
interval."
RL Genomics 60:137-151(1999).
RN 14
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN-129/SV:
RX MEDLINE=97131520; PubMed=8975718;

Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
Kunkel L.M., Dietrich W.F.;
"the mouse region syntenic for human spinal muscular atrophy lies
within the Lgn1 critical interval and contains multiple copies of Nalp
exon 5."
Genomics 38:405-417(1996).
-1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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CC -----
CC EMBL: AF135489; AAD56761.1; -
CC EMBL: AF135490; AAD56762.1; -
CC EMBL: AF102871; AAC73002.1; -
CC EMBL: AF131205; AAD56759.1; -
CC EMBL: U66329; AAC52977.1; -
CC HSSP: Q13490; 108H
CC MGD: MGI:1298226; Birc1b.
CC InterPro: IPR001370; BIR.
CC Pfam: PF00653; BIR.
CC SMART: SM00238; BIR; 3.
CC PROSITE: PS01282; BIR_REPEAT_1; 2.
CC PROSITE: PS01443; BIR_REPEAT_2; 3.
CC PROSITE: PS00837; NACHT; 1.
CC Apoptosis: Repeat; Multigene family.
CC REPEAT 159 227 BIR 1.
CC REPEAT 278 345 BIR 2.
CC DOMAIN 508 802 BIR 3.
CC CONFLICT 377 377 NACHT.
CC CONFLICT 403 403 D -> G (IN REF. 3).
CC CONFLICT 478 478 L -> F (IN REF. 3).
CC CONFLICT 540 540 N -> Y (IN REF. 3).
CC CONFLICT 862 862 K -> N (IN REF. 3).
CC CONFLICT 1079 1080 SD -> FN (IN REF. 3).
CC CONFLICT 1089 1089 R -> C (IN REF. 3).
CC CONFLICT 1115 1115 K -> E (IN REF. 3).
CC CONFLICT 1122 1122 T -> A (IN REF. 3).
CC CONFLICT 1136 1136 D -> E (IN REF. 3).
CC CONFLICT 1157 1157 S -> G (IN REF. 3).
CC CONFLICT 1167 1167 G -> R (IN REF. 3).
CC CONFLICT 1271 1271 F -> C (IN REF. 3).
CC SEQUENCE 1447 AA; 164033 MW; 9EF6C6A73BAE60A2 CRC64;

Query Match 67 38; Score 4919; DB 1; Length 1447;
Best Local Similarity 65.4%; Pred. No. 4,4e-284;
Matches 946; Conservative 180; Mismatches 277; Indels 44; Gaps 2;
OY 1 MATOKASDERISOFDHNLLPELSALIGDAVOLAKLEEEPOKRAMQGVNSQRSE 60
Db 1 MAOGEAEEVEELICEFDDDLIVSELSTLRVDALSVAKROOEDHRTKMKKGFSQMRSE 60
OY 61 AKRLKFTVTEPEYSWIPOMAAAGFYTFGVKSGIQCCSLIFGAGLTRLPJEDHKRP 120
Db 61 AKRLKFTVTEPEYSWIPOMAAAGFYTFGVKSGIQCCSLIFGAGLTRLPJEDHKRP 120
OY 121 HPDCGFLNKKDKGNIAKIDIRVKNLSRLRGKMYOESEARLASPNMFFYOGISPCV 180
Db 121 HPDCGFLNKKDKGNIAKIDIRVKNLSRLRGKMYOESEARLASPNMFFYOGISPCV 180
OY 181 L5DAGVFTGKODTVQCCSGCGCIGNNEEGDDPKKEHAKWFPCEFLRSKSSSEITQYI 240
Db 181 L5DAGVFTGKODTVQCCSGCGCIGNNEEGDDPKKEHAKWFPCEFLRSKSSSEITQYI 240
OY 181 L5AAGVFTGKRDVYQCCSGCGCIGNNEEGDDPKKEHAKWFPCEFLRSKSSSEITQYV 240
Db 181 L5AAGVFTGKRDVYQCCSGCGCIGNNEEGDDPKKEHAKWFPCEFLRSKSSSEITQYV 240

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```

Qy 241 QSYKGVDTITGEHFNVSNOVELPMASAYCNDISIFAYEEELRDSFKDMPRESAVGVAALA 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSYEGFLLHTGHEFNVSWMRRELPMSAYCNDISVAFNEBELRMDTFRKDPHESPGVAELV 300
Qy 301 KAGLEFYTGKIDVOFCSCGGCLEKQEGDDPLDDHTRCFPKPCPIQNNKSSAEVTPDLOS 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 KAGLEFYTGKIDVOFCSCGGCEKMEKAGDNPJEDHTKEFPNCVFLQTLKSSAEVIALPOS 360
Qy 361 RGELEFETTESNLEDSIAY----- 382
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 HCALPEAMETTESNHDPAAHSTVVDVSPSEAOELEBPASSLVLCRDDHSPAQGRG 420
Qy 383 ----GPIVP--EMAGGEAQMFOEAKNLNEOLRAATYSAFRMSLIDISSDLATDHLGC 436
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 421 CASSTGYLPSPDLDGSEAKWLOEARSLSBQLRDYTKATFRMNPPEVYSLGTHLLSC 480
Qy 437 DLSIAKSIKRPVQEPPLVPEYFGMLNSVCEGAGSGKTVLLKIAFLMAAGCCPLLN 496
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 DVSIIKSHISQPVQSLTIPVEFMSLNSVMCEGAGSGKTFKRIAFMAAGCCPLLN 540
Qy 497 RFOLEFYLSTSTRDEGLASTICDQLLEKESVTCEMCRNTIIOOLKNVLFLLDYKEI 556
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 RPOLVFTYLSSTITPGOELAKITCAQLGAGGCISEVCLSTIIOLOHGVLEFLDDYSGL 600
Qy 557 CSIPQVIGKLIQKNHLSFTCLIAVRTNRARDIRRYLETILEIKAFPPYNTVCILRKLF 616
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 ASLPQALHTLTITKNVLSFTCLIAVHTNKVRIGIRYLDTSLEIKFPPYNTVSVLRKLFS 660
Qy 617 HNMTRKRFMYFGKNOSLOKTPPLVYALICAMFQYPPDPSPDDYAVKSYMERLSL 676
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 HDIMVNRKFINFGHEELQGIHKTPLEVAACVTDMFNPSQAPQDALFKAYMOYLSL 720
Qy 677 RNMKATAEIKATVSSCGELATLKGFFSCCFEENDDDLAEGVDEDDLMCLSKFTAORL 736
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 KHKGAAPLOATVSSCGOALATLGLFSSCFEPNSDLAEGVDEDELTCLMSKTAORL 780
Qy 737 RPEYFELSPAFOELAGKRLIELDSDROHODLGLYHLKOINSPMTVSAVNNFLNYS 796
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 781 RPYVFLPLPFOELAAVRLTELSSDROEDDGLLYLRQJNSLKLKMSIHYFLTKYVS 840
Qy 797 SLPSKAPKIVSHLLHVDNKESENSENDYLRKHOPEISLOQLRLGMLQICPOAYF 856
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 841 SHPSKAPVAVSHLOLVDEKESLENMSEMEDYKMLRHEALMTECRLGMLQSLPESFS 900
Qy 857 SWSVSHLVIALKTAYOSNTVACSPYLOFLOGRITLTGALNTLYFDPHPSLSLSLSI 916
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 901 LFLISNLRICLNFAHESNTVACSPVLLQFLGRITLDKVTSLQYFMDHPETLLLLLSI 960
Qy 917 HEPFIRKNTSPRAHPSVLETCFDSQVPTIIDODVSAFEPNEMERNLAEKEDNVKSYMD 976
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 961 KISLGNMNVQRIIDFSLIEKSPKQVOPPTIIDODVAIAFOPINEVOGNLSEKKHIIKKYED 1020
Qy 977 MQRASPSDLSGYWKLKSKYKIRPCLEVDYNDIDVVGDMLEILMTVVSASRIELHLNH 1036
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1021 MKHQPLPLNISTGYWKLSPRPYKIPLEVQVNTGPADALLQVLEVVSASQISIEFRLSD 1080
Qy 1037 SSGFTESTIRPALELSKASVTKCSISKLELSAEQELLTLPLSLELEVSQTOSODQTFP 1096
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1081 SSGFTESTIRPALELSKASVTKCSMRLELSRDOKLLTLPLTQLELEVSQTNLDQFLPH 1140
Qy 1097 NIDKFLCKLELSVDLEGNINVSFVPEERPNFHEMKELLIQISABYDSKVLKLIQNSPN 1156
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1141 NIAHKLGLKELCVRLDSRPDVLVLPGEFPNLHMEKLSIRFSTSDLSKLILQNSPN 1200
Qy 1157 LHVFLKCNFSDGSLMTMLVSCKKLTKIKFSDFQAVPVPVVALPFIISKIINTLEQ 1216
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1201 LHVFLKCNFSDGSLMTMLVSCKKLTKIKFSDFQAVPVPVVALPFIISKIINTLEQ 1260
Qy 1217 QPPDEETSEKFAVILGSLNLEELIPLTGDGIYRAKALIQOCCOOLHICRVLSPFKTLD 1276
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1261 QPPDEETSEKFAVILGSLNLEELIPLTGDGIYRAKALIVRCLOLPCILRVLPFETLDD 1320
Qy 1277 DSVVEIARVAISGFOKLENLKLSINHKTTEBGRNFTQALDNMNLQELDISRHFTECI 1336

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Db 1321 DSVLEIARAGATRGFOKLENLIDLTLNKHKTTEBGRNFTQVLDNPLNKLNDISRHIPCI 1380
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    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1381 QIOATVVALGOCVSRPLSLRLGLMSLWLBDEEDIKVINDKERRHPOSRLTVHWRVVP 1440
Qy 1397 FSPITOK 1403
    |||:|||||
Db 1441 FSPVIOK 1447

RESULT 4
BIRE_MOUSE
ID BIRE_MOUSE STANDARD; PRT: 1403 AA.
AC Q9R016; Q9R029; P81703; 009122; 009121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
inhibitory protein 5).
GN BIRC1 OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431676; PubMed=10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "Type mouse Naip gene cluster on Chromosome 13 encodes several distinct
functional transcripts."
RL Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV;
RC MEDLINE=99417674; PubMed=10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunkel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Iap1/5MA
interval."
RL Genomics 60:137-151(1999).
RN [3]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/SV;
RC MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Iap1 critical interval and contains multiple copies of Naip
exon 5."
RL Genomics 38:405-417(1996).
CC - FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
CC - SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
CC EMBL: AF135492; AAD56764.1; -
CC DR EMBL: AF131205; AAD56760.1; -
CC DR EMBL: U66326; AAC52974.1; -
CC DR HSSP: Q13490; 10BH.
CC DR MGP: MGI:1298220; Birc1e.
CC DR InterPro: IPR001370; BIR.
CC DR Pfam: PF00653; BIR; 3.
CC DR SMART: SM00238; BIR; 3.

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DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS50837; NACHT; 1.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60  
 FT REPEAT 127  
 FT REPEAT 159  
 FT REPEAT 227  
 FT REPEAT 278  
 FT REPEAT 345  
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 FT REPEAT 759  
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 FT REPEAT 1129  
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 FT REPEAT 1403  
 AA: 159695 MW: B27F645043BC642 CRC64;

Query Match 66.8%; Score 4885; DB 1; Length 1403;  
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 Matches 947; Conservative 167; Mismatches 286; Indels 2; Gaps 2;

QY 1 MATOOKASDERISOFHNLPELSALLGLDANOLAELEBOKERAKKQKQNSOMSE 60  
 DB 1 MAHGESSEDRISIDIEFELPELSALLGLDANOLAELEBOKERAKKQKQNSOMSE 60  
 QY 61 AKRKTFTVTPEPYSWIPQEMAAGFYFVGVSGLQCFCCSLILGALTLRLPTEDHRRF 120  
 DB 61 AKRKTFTFTDTRSTWPEMAAAGFYHGVGLVQCCCSLILGNSLRPLTERHKL 120  
 QY 121 HPDCGFLNKDVGNIKYIIRVKNLSRGRKMYOEDEARLASFRNMPFYVGISPCV 180  
 DB 121 RPCEFLGKDNVGNIKYIRKSPKMLRGKARYHEEERALSFEDEMPYANGTSRV 180  
 QY 181 LSPAGFVFGKDDTVQVCGSCGGLGNMBEGDDPMKEHAKMPKCEFLRSKSSSELTQY 240  
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 QY 241 QSYKGFVDITGEHFNNSWVORELPMASVYNDSTFATYELRLDSFKWMPRESAVGAALA 300  
 DB 241 QSYEGFVHTGEHFNNSWVORELPMASVYNDSTFATYELRLDSFKWMPRESAVGAALA 300  
 QY 301 KAGLFYTGKIDYVCFSCGGLCEKWOEGDDPLDHTRCFNPCEFLDNMKSAAVPPDLOS 360  
 DB 301 KAGFYTGKIDYVCFSCGGLCEKWOEGDDPLDHTRCFNPCEFLDNMKSAAVPPDLOS 360  
 QY 361 RGEIJJLETTSESNLEDSIAVGPVPEMAOGAOMFOEAKNLNEQLRAAYTSASFRIHMS 420  
 DB 361 RGEIJJLETTSESNLEDSIAVGPVPEMAOGAOMFOEAKNLNEQLRAAYTSASFRIHMS 420  
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 QY 481 KRIAFIWAASCCPLNRFOLVFLSTSTRPREGIASSITCDOLLEKESVTEMCRNIQ 540  
 DB 481 KRIAFIWAASCCPLNRFOLVFLSTSTRPREGIASSITCDOLLEKESVTEMCRNIQ 540  
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 DB 541 QLNKQVFLLDYKKEICSPVOTGKLOKNIHSFRLIIVARTRARIRRYLETILEIK 600  
 QY 601 AEPFNTVYICLRKLFNSHMTRLRKFMVYEGKNSLOKIQKTPYFAVIAICAHMFQ-YFPDP 659  
 DB 601 AEPFNTVYICLRKLFNSHMTRLRKFMVYEGKNSLOKIQKTPYFAVIAICAHMFQ-YFPDP 659  
 QY 660 SPDDVAVAKSWERLSLNKATAEILAAVSSCGELAKGFFSCCFEFDNDOLAAGVDE 719  
 DB 660 SPDDVAVAKSWERLSLNKATAEILAAVSSCGELAKGFFSCCFEFDNDOLAAGVDE 719

DB 661 KFDQVTLFQSYQWYLSTKATKATAEPLQNTVSSCCOLATGLTFSSCFEFDNDOLAAGVDE 720  
 QY 720 DEDIFMCMSKRTAORLRPRYRFLSPAFQEFIAQMRLEILLDSROHODLGTYHKOIN 779  
 DB 721 DEKTLTLMSKRTAORLRPRYRFLSPAFQEFIAQMRLEILLDSROHODLGTYHKOIN 780  
 QY 780 SPMTVAVYNNFLNVSSLPSTKAGPKIVSHLHLVYKNSLENISEBNDYKHOPEISL 839  
 DB 781 SPLKAINSFNIFLYVSSSHSSKAPVYVSHLQLDKESKLENISEBNDYKHOPEISL 840  
 QY 840 QMOLLRGMOICPAYGSMVSEHLVYALKTAVQSNVAVASCFFVLOFLQRTGLTGLN 899  
 DB 841 WQFVGRGLMVLSPSSSVSEHLRLALIFYAESNTVAVSCSPFIQLRGRTTLARVLN 900  
 QY 900 LQYFDDHRESILSLRSIHPRGNKTSIPRAHFVLETCEDSKQVPIQODVYASAFEPNE 959  
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 QY 960 WERNIAEKEDNVKSNQMDORASPDLSITYWKLSPKQYKIPCLLEVANDVIDVYQDMLEI 1019  
 DB 960 WRRNFADDEELIKNTYERIRALPDISEGYWKLSPKPKIPKLEVQVNNTOADQALQV 1019  
 QY 1020 LMTVFSASORIELHLNHSKGTESIIRPALELSKASVTKCSISKELSAEOELLTLPSL 1079  
 DB 1020 LMEVFSASOIEFRILPNSGFLIESICPALELSKASVTKCSMSRLELSAEOELLTLPAL 1079  
 QY 1080 ESLEVSCTIOSDDQIFPNLDKFLCKEISVDLEGNINVSFYIPEFPNHHMEKLLTOIS 1139  
 DB 1080 OSLEVSCTIOSDDQIFPNLDKFLCKEISVDLEGNINVSFYIPEFPNHHMEKLLTOIS 1139  
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 DB 1140 TESDSLKLVKFIQNPVNLHVFLKCNFPSPDPSLMTJMYGSKLTKTEKFSDFQAVPV 1199  
 QY 1200 ASLPNFSILKILNLEGOQFPEETSEKFAIYLSLWLEELIPTDGGIYRAKLIQOC 1259  
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 DB 1260 LQPLCLRLVSLFFKTLNDSVVEIAKVAISGFORLENTKLSINHKTTEGYNPFQALDN 1319  
 QY 1320 MPNLQELDISRHFEETCKAOTVKSISOCVYLRPLRLINLNSWLDDADDAIALNVKKE 1379  
 DB 1320 LPNQELDISRHFEETCKAOTVKSISOCVYLRPLRLINLNSWLDDADDAIALNVKKE 1379  
 QY 1380 RHPOSKYTLTLQKWLIPFSPFI 1401  
 DB 1380 RHPOSKYTLTLQKWLIPFSPFI 1401

RESULT 5  
 BIRF\_MOUSE  
 ID BIRF\_MOUSE STANDARD; PRT; 1403 AA.  
 AC 09JTB6: P81704; 009122; 009121;  
 DT 16-OCT-2001 (rel. 40, Created)  
 DT 16-OCT-2001 (rel. 40, Last sequence update)  
 DT 01-MAR-2002 (rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 1f (Neuronal) apoptosis  
 GN Inhibitory protein 6.  
 GN BIRCF1 OR NAIP6 OR NAIP-RS4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RX MEDLINE=20414747; PubMed=10958627;  
 RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.:  
 FT "Genomic sequence analysis of the mouse Naip gene array.";  
 RL Genome Res. 10:1095-1102(2000).  
 RN [2]



RP SEQUENCE OF 82-168 FROM N.A.  
RC STRAIN-129/SVJ:  
RX MEDLINE-97131520: PubMed-8975718:  
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,  
Kunkel L.M., Dietrich W.F.:  
RT "The mouse region syntenic for human spinal muscular atrophy lies  
within the 1q91 critical interval and contains multiple copies of Nalp  
exon 5.";  
RL Genomics 38:405-417(1996).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC STIMULS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
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CC -----  
DR EMBL: AF242431: AAF82751.1: -  
DR EMBL: U66327: AAC52975.1: -  
DR MGD: MG1:1298222: BIRclt.  
DR InterPro: IPR001370: BIR.  
DR Pfam: PF00653: BIR: 3.  
DR SMART: SM00238: BIR: 3.  
DR PROSITE: PS01282: BIR\_REPEAT\_1; 2.  
DR PROSITE: PS0143: BIR\_REPEAT\_2; 3.  
DR PROSITE: PS50837: NACHT: 1.  
KW Apoptosis; Repeat; Multigene family.  
FT REPEAT 60 127 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT DOMAIN 464 NACHT.  
SQ SEQUENCE 1403 AA: 159823 MW: 9DA912503358C4E9 CRC64:  
  
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Best Local Similarity 66.3%: Pred. No. 1,1e-277;  
Matches 925: Conservative 174: Mismatches 237: Indels 2: Gaps 2:  
  
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QY 61 AKRLKLTFTYTPYSSWLPQEMAAAGFTYGVKSGIQCCSLLIFGAGLPTIEDHKRF 120  
DB 61 AKRLKLTFTYTPYSSWLPQEMAAAGFTYGVKSGIQCCSLLIFGAGLPTIEDHKRF 120  
QY 121 HPDCGFLNKNVGNIAKIDIVKLNLSKRLRGKMKRYOEEEARLASFRMPPYVGISFCV 180  
DB 121 RPEEFELQGRKVGNGIKGIDIVKSPKMLRGKAKARYHEEERKLESFEDMPYTAGSTFRA 180  
QY 181 LSEAGFVFTGKQDVTQFCSCGCLGNMEEGDDPKKEHAKMPKCEFLRSKSSSEETIYI 240  
DB 181 LSAAGFVFTGKQDVTQFCSCGCLGNMEEGDDPKKEHAKMPKCEFLRSKSSSEETIYI 240  
QY 241 QSYGFDVDTGEHFNVSQVRELPMASAYCNDISFAIEELRLDSFKMPRESAVGVALA 300  
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DB 301 KAGLPYGIKIDVQFCSCGCLGKMOEGDDPLDHTRCFPCPFLONNKSSAEVTPDLOS 360  
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QY 421 LLDISSDLATDHLGCDLSTSKHISKVPQEPVLPVPEFGMLNSVMYCEGAGSGKTVLL 480  
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QY 481 KKIATLMAAGCCPPLNRRQVLYLSLSTRDEGLASITCDOLKEGSEVTEMCRRNIIQ 540  
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DB 541 QLNQVLLDLDYKEIGSIPQVIGKIQNHLSFCCILIAVTRNARIDRLEFLEIFK 600  
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QY 660 SPDDVAVRSVNERLSLNKKAETLKATVSSCGGLAKGFFSCCFERNDDILAAGVDE 719  
DB 660 SPDDVAVRSVNERLSLNKKAETLKATVSSCGGLAKGFFSCCFERNDDILAAGVDE 719  
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DB 720 DEDLTMCMSKFTAAQLRPFYRFLSPAFOEFLAGRLIELDSDRQEHODGLYHLAKQIN 779  
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DB 721 DYKLTTFPLMSKRTAQLRPVYRFLQPLQEPFLAARLRELLSSDRQEDQDGLYLRQID 780  
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DB 780 SPMAVTSAYNNFLNVTSSLPSTKACPKIVSHLHLVDNKESELENISENDVYKHOPEISL 839  
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DB 840 QMQLLRGLMOICPOAFVEMVSEHLLVLKTRAYOSNTVAAAGSPVYQLOQRTLTGLN 899  
QY 900 LOYFFDHPESLILRSIFPIRGNTSPRAHPSVLETQCFDSQVTPQODVAAASAPNE 959  
DB 900 LOYFFDHPESLILRSIFPIRGNTSPRAHPSVLETQCFDSQVTPQODVAAASAPNE 959  
QY 901 LEYFDHDESLILRLSLKSVINGKMSYVDYS-FKTFENLQPAINEETISAEHVSE 959  
DB 901 LEYFDHDESLILRLSLKSVINGKMSYVDYS-FKTFENLQPAINEETISAEHVSE 959  
QY 960 WERNIAEKEDVNVKSYMQRASPDLSGTYMKLSKROYKICPLEVDVNDIDVYGOMLEI 1019  
DB 960 WERNIAEKEDVNVKSYMQRASPDLSGTYMKLSKROYKICPLEVDVNDIDVYGOMLEI 1019  
QY 1020 LMTVFSASORIEIHNHSGFPESTRPALDELKASVTGCSISKLELSAABDELLTLPSL 1079  
DB 1020 LMTVFSASORIEIHNHSGFPESTRPALDELKASVTGCSISKLELSAABDELLTLPSL 1079  
QY 1080 ESLEVSGTIOQODQIFPMLDKFLCKELSVDELGNINVFSSVYPEEFPNHHHEKLLIOIS 1139  
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DB 1200 ASLPNFIKLTILNLEGGQFPPEETSEKFAVTLGSLSNLELILPFGDITVRAKLIIOOC 1259  
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QY 1380 RHPOSXYTITIQKWLTPSPPII 1401  
DB 1380 RHPOSXYTITIQKWLTPSPPII 1401  
  
RESULT 6  
BIRG\_MOUSE STANDARD: PRT: 1402 AA.  
ID BIRG\_MOUSE  
AC 0901B3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
GN BIRC1G OR NAIP7).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Gromey J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL: AF242433; AAF82749.1;
DR MCD: MG11858256; Birc1g.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50837; NACHT; 1.
DR APOPTOSIS; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA; 159662 MW; CIDFBA359893E0D CRC64;

Query Match 65.68; Score 4796.5; DB 1; Length 1402;
Best Local Similarity 66.48; Pred. No. 7.9e-277;
Matches 931; Conservative 171; Mismatches 297; Indels 3; Gaps 3;

QY 1 MATOQKASDERISQFDHNLPELISALLGLDAVOLAKELLEEOKERAKQKQKYNQOMSE 60
DB 1 MAHGESEEDRISIDIEFLAELISARGMNLVOLAKSDEEDHKEKRMKKGPNQOMSE 60
QY 61 AKRLKTVTEPYESSYLPOEMAAGFYFTGVSGIOQCCSLILFGACULRPTEDHKRF 120
DB 61 AKRLKTVTEPYESSYLPOEMAAGFYFTGVSGIOQCCSLILFGACULRPTEDHKRF 120
QY 121 HPDQGLLNKNDVGNIAKIDIRVKNLKSRLRGKMKRYOEERARLASFRNMPYVGISPCV 180
DB 121 RPECEFLQGDVGNICKYDIRVKSPEKMLRGKAKARYHEERARLESFEDWPEYAGTSFV 180
QY 181 LSEAGVFTGKDTVOGSCGCGCLNMEGGDPWKENAKMFPKCEFLRSKSKSEETQYI 240
DB 181 LSEAGVFTGKDTVOGSCGCGCLNMEGGDPWKENAKMFPKCEFLRSKSKSEETQYI 240
QY 241 OSYKGFVDTGTHFVNSVWORELPMASAYCNDSEFAYEELRLDSFKDMPRESAVGVALA 300
DB 241 OSYKGFVDTGTHFVNSVWORELPMASAYCNDSEFAYEELRLDSFKDMPRESAVGVALA 300
QY 301 KAGLEFYGIRKIVOCFCSCGCLLEKMOGDDPLDDHTRCFENCFPLDNMKSASAEVPPDLS 360
DB 301 KAGLEFYGIRKIVOCFCSCGCLLEKMOGDDPLDDHTRCFENCFPLDNMKSASAEVPPDLS 360
QY 361 RGELELLETTSESNLDSIAGVPIVPEMAQGEAOMFOAKMLNEQLRAAYTSASFRRMS 420
DB 361 RGELELLETTSESNLDSIAGVPIVPEMAQGEAOMFOAKMLNEQLRAAYTSASFRRMS 420

DB 361 QVALPEATEETRESNNGAAVHSTFVDLGRSEAQMFQEARSLSEQRLDYTTSTSCHN 420
QY 421 LDDISSDLATDHLCCDLSIAKSHISKRPQEPFLPVPFGNLSVNCVEGASGCTVLL 480
DB 421 LREVCSSLTQDHLSCDVSIIKSHISQVQCALTPPEVFSNLSVNCVEGASGCTVLL 480
QY 481 KRIAFILMASGCCPLLRQALRYFVLSSTRDEGLASIIQDLEKEGVTEKQMNIIQ 540
DB 481 KRIAFILMASGCCPLLRQALRYFVLSSTRDEGLASIIQDLEKEGVTEKQMNIIQ 540
QY 541 QLNQVFLPLDDYVEIGSIFQVIGIKLOKNHLSRTCLLAFTNRNRDRRLTLEIK 600
DB 541 QLNQVFLPLDDYVEIGSIFQVIGIKLOKNHLSRTCLLAFTNRNRDRRLTLEIK 600
QY 601 APEPYNTVCLRLKFSHNMRKRPVYTGKQKQSLQKTPFLFAALCAHFO-YRDP 659
DB 601 APEPYNTVCLRLKFSHNMRKRPVYTGKQKQSLQKTPFLFAALCAHFO-YRDP 659
QY 660 SFDDVAVFKSYMERLSLRNKAATAEILKATVSSCGELALGFSCCFERNDDLAAGVDE 719
DB 660 SFDDVAVFKSYMERLSLRNKAATAEILKATVSSCGELALGFSCCFERNDDLAAGVDE 719
QY 720 DEDITNCLSKFTFAQRLRFYRFLSPARQEFLAGRLIELDSDROBODLGLYHKOIN 779
DB 720 DEDITNCLSKFTFAQRLRFYRFLSPARQEFLAGRLIELDSDROBODLGLYHKOIN 779
QY 780 SPMTATVSNANFLNVLSSSLPSTKAPKIVSHLALVNKESLENISNDYTKHOREISL 839
DB 780 SPMTATVSNANFLNVLSSSLPSTKAPKIVSHLALVNKESLENISNDYTKHOREISL 839
QY 840 QNQLRGIMQICPOAYFSVMSEHLLVALTAVQSNVNAACSPFVLOTLQRTLTGALN 899
DB 840 QNQLRGIMQICPOAYFSVMSEHLLVALTAVQSNVNAACSPFVLOTLQRTLTGALN 899
QY 900 LQYFEDPESELISLRSHPIRGNKTSPPRANHSVLETCQSOVPTIQQDYSAEPNNE 959
DB 900 LQYFEDPESELISLRSHPIRGNKTSPPRANHSVLETCQSOVPTIQQDYSAEPNNE 959
QY 960 WERNLAKEDNVASYNDMORRASPDLSTGYMKLSPROXYRIPCELDVAVNDIVYQDILEI 1019
DB 960 WERNLAKEDNVASYNDMORRASPDLSTGYMKLSPROXYRIPCELDVAVNDIVYQDILEI 1019
QY 1020 LMEVFSASQIEPHILFNSGFLSTIRPALELSKASVTKCSMRLELSRAQDELLTLPAL 1079
DB 1020 LMEVFSASQIEPHILFNSGFLSTIRPALELSKASVTKCSMRLELSRAQDELLTLPAL 1079
QY 1080 ESELEVGCTIQSDQIFPNLDFLCLKELSYDLEGNINVFSTYPERPNHMKLLIQIS 1139
DB 1080 ESELEVGCTIQSDQIFPNLDFLCLKELSYDLEGNINVFSTYPERPNHMKLLIQIS 1139
QY 1140 AEYDPSKLVKLQNSPNLHVFLHCNFPSPDGLMTVLVSCCKLTKIKTSDFFOAVPFV 1199
DB 1140 AEYDPSKLVKLQNSPNLHVFLHCNFPSPDGLMTVLVSCCKLTKIKTSDFFOAVPFV 1199
QY 1200 ASLPNFSILKLNLEGOQFDEPTESEKFAVILGSLNLEELILPTDGGIYRAKIIQOC 1259
DB 1200 ASLPNFSILKLNLEGOQFDEPTESEKFAVILGSLNLEELILPTDGGIYRAKIIQOC 1259
QY 1260 QQLHCLVLSFFKTLANDSVYELAKVAISGGFOKLENLKLSINHITTEGYRNFFOALDN 1319
DB 1260 QQLHCLVLSFFKTLANDSVYELAKVAISGGFOKLENLKLSINHITTEGYRNFFOALDN 1319
QY 1320 MPNLQELDISRHFTECIKQATTVKSLSCVLRPLRLNMLNSWLDADADIALNLMKE 1379
DB 1320 MPNLQELDISRHFTECIKQATTVKSLSCVLRPLRLNMLNSWLDADADIALNLMKE 1379
QY 1380 RHPOSKYLTLLQKMLPESPPII 1401
DB 1380 RHPOSKYLTLLQKMLPESPPII 1401
QY 1379 RHPOSKYLTLLQKMLPESPPII 1400
DB 1379 RHPOSKYLTLLQKMLPESPPII 1400

RESULT 7
CARC_HUMAN

```



Db 440 KFFHKSQEVYAGRLSSLLTSHPEEYTKGCVLQKWSISDITSTYSSILRTCCSSV 499  
 QY 799 PSTKAGPKIVSHLLHLYDN-----KESLENTSENDYLLKHQPELSIQMOL 843  
 Db 500 EATRA---VVKHLAAVYQGLGSLIAKRLPLMQESLSQVKN-----TTEOEI 545  
 QY 844 LRGLMVICQVAFSNVSEHLVLAUKTAVQGNF--VAACSPVYLOFLOGRTLTGALNTL-Q 901  
 Db 546 LKAI-----NINSFVECGIHL-----YQSTSKSLSEQFAFPQGSLEYINSGNIPD 593  
 QY 902 YFPDHPESLSLSTRTHFPIRGNKTSPPRHFSVLETCQKDSQVPTIDQVASFEPNME 961  
 Db 594 YLFD-----FEHLPCN--ASALDFIKLDFYGG--AAASWE 625  
 QY 962 RNLAKEEDNVKASYMDQRRASPDLSTGYWKLSPKQYKIP-----CLEYDV 1006  
 Db 626 -----KAEEDTGGIHMDEAPETY-IPSRVSLPFPMKQEPFTLEVT 666  
 QY 1007 NDIDVQGDMLILMTVFSASQRIEHLNHSRGTESIRPALESKASVTGCSISKLELS 1066  
 Db 667 RDSFKLKKODIRYLKIFSSATSLRLQIRKCGVAGSLVLSYCK-NIYSLVLEASPLR 725  
 QY 1067 AADQELLTLPSLESLEVGSTIQSDQIFPN--LDKFLCLKELSVDEGNINFEVTPPE 1124  
 Db 726 IEERRHITSYTNLKTLSH---DIQNRPLFGGLTDSIGNLKTLKLMQNIKA----- 775  
 QY 1125 FPFHMERKLLQISAEVDPSKVLKLSNPNLHVFLKCNFSDSGSLMTMLVS----- 1179  
 Db 776 -----NEEDAIKLAEGKLNKLMCLPHL--THLSDGEGMDVYLSLSE 818  
 QY 1180 -CKKLETKFSDSEF--QAVPFVA-SLPNFSIKLTLNEGQFPDEETSEKFAVILGSLIS 1235  
 Db 819 PC-DIEETQLVSCCLSANAAVKILQNLHNLVNLKLSIDL--SENYLEKQEGNALHELIDMAN 876  
 QY 1236 NLEE---LILPTGDIYRAKVLIIQCCOHLCLRVLSFEKTLNDSEVIAKVAISGF- 1291  
 Db 877 VLEQUTALMLPWCQDVQGSLSLKLHLEVPOLVYKLGKLNMRHDP-----EIRILDAFF 931  
 QY 1292 -----QKLEMLKLSINHKTTEEGYRNFQALDNMNPLOELIDISRHTECIRKATQYKSL 1346  
 Db 932 CKNPMLKFPQDLNLAGN-RVSSDGMVLAFMGVENLQQLVFFDS---TKERPLPALVRYKL 987  
 QY 1347 SCQVLRPLRLIRLMLSMVLLDADIDALL 1374  
 Db 988 SOVLSKLTFLEQEARLYVGMQFDDDLSTV 1015  
 RESULT 8  
 BIR3\_HUMAN STANDARD: PRT: 618 AA.  
 AC 013450: 016516;  
 DT 01-NOV-1987 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (IAP repeat-containing protein 3) (C-TIAP1) (TNFR2-TNFR signaling complex BIRC3 OR AIP2 OR IAP2 OR MIHB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96126127; PubMed=8548810.  
 RA "The TNFR2-TNFR signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins."  
 RT Cell 83:1243-1252(1995).  
 RN  
 RP  
 RC  
 RX MEDLINE=96149249; PubMed=8552191;

RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,  
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Koroluk R.G.;  
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
 RL family of IAP genes."  
 RN Nature 379:345-353(1996).  
 RP  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal liver;  
 RX MEDLINE=96209843; PubMed=8643514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
 RT "Cloning and expression of apoptosis inhibitory protein homologs that  
 RT function to inhibit apoptosis and/or bind tumor necrosis factor  
 RL receptor-associated factors."  
 RN Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 RP  
 RP STRUCTURE BY NMR OF 266-363.  
 RX MEDLINE=9932054; PubMed=10404221;  
 RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
 RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
 RT repeat."  
 RL Nat. Struct. Biol. 6:648-651(1999).  
 CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Potentially).  
 CC -I- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.  
 CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
 CC AND PANCREAS. LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
 CC LEUKOCYTES.  
 CC -I- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -I- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -I- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch).  
 DR EMBL: I49431; AAC41942.1;  
 DR EMBL: U45879; AAC50372.1;  
 DR EMBL: U37547; AAC50508.1;  
 DR PDB: 1OBH; 20-OCT-99.  
 DR MIM: 601721;  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; Znf\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS01463; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS0209; CARD; 1.  
 DR PROSITE: PS00518; zf\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS00089; zf\_RING\_2; 1.  
 KW Apoptosis; Zinc-finger; Repeat; 3D-structure.  
 FT REPEAT 46 113  
 FT REPEAT 184 250  
 FT REPEAT 269 336  
 FT REPEAT 453 543  
 FT ZN\_FING 571 606  
 FT CARD 157 157  
 FT CONFLICT 157 157  
 FT CONFLICT 308 308  
 FT CONFLICT 414 414  
 FT CONFLICT 514 514  
 FT SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;



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Db 251 RES-----ISNLSMOTHSARLRFLYMPSPVPV 278
Qy 295 GVALAKAGLFTYGIKDIYOCFSCGGLKEMOBDPLDHPNCFNCPFLONMSSAEV 354
Db 279 QPEOLASAGFYTVYRNDVAKFCFCCDGLRCMEGDDPMLEHAKWPFRCFELRMGO--EF 337
Qy 355 TPDIQSR-GEICELLETTESNLEDSTAVGPIYVEMAOEACQFOEAKNLNFOILMAATS 413
Db 338 VDEIQARYPHLEQLLSTSDTPPEENADPTETVYHFGPE-----SS 379
Qy 414 ASFRHMSLIDISDLTDHLGCDLSIAKHSKIPVOPVLYPEVFGNLVSMGV-----E 469
Db 380 EDVYMMSTPVYKALE-----KGFSSRLVQOTVOROI---LATGNYRTVNDIVSLLNAE 432
Qy 470 GEAGSGKTYLKKIAFLMASGCCPLNRFOLYFVLSSTSPDGLASITCDQLLEKGS 529
Db 433 DEEREERK---ERQTEEMASGDLSTLRKNRMALFOOLTHVLP-----ILDNLL--EAS 480
Qy 530 VTEMCMRNITIOOLKNQV 546
Db 481 VITKQEHDIIRQ-KTOI 496

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RESULT 10
BIR2_MOUSE
AC 008863; STANDARD; PRT; 600 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis protein 1) (MIRP1) (MIRAP-1).
GN BIRC2 OR API1 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liscion P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes.
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC EMBL: U88908; MACE53531.1;
DR HSRP: Q13490; IOBH.
DR MGD: Q13490; IOBH.
DR InterPro: IPR001370; BIRC2.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_C1ng.
DR Pfam: PF00653; BIR3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; ZF-C3HC4; 1.
DR SMART: SM00238; BIR; 3.

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DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00869; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger Repeat.
FT REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN_FING 553 588 RING-TYPE.
SO SEQUENCE 600 AA; 67198 MW; ADVF73E6849317D1 CRC64;

Query Match
Best Local Similarity 6.0%; Score 440; DB 1; Length 600;
Matches 145; Conservative 88; Mismatches 226; Indels 162; Gaps 19;

Qy 47 AKMOKGYS-----QMRSEAKRLKTFYTYEPYSSMIP---QEMAAAGFYTVGKSGIOCF 98
Db 9 AKLMKSADTFELKYDFSCELYRLS---TYSAPFGVPSVSESLARAGFYTVGANDVKCF 65
Qy 99 CCSLILFAGLRLPIEDHKRPHDCGFLNKGDNIAKYDIRKYNLKSRLBGKMY-- 156
Db 66 CCGMLDMNKKQDSSPMENHRKRLYPCNFVOTLNPANSLASPPSLPSTAMSTMPLEFNS 125
Qy 157 -----QEEARLASRNNPFFVOGTS 177
Db 126 SENTGFSGSYSPSPDPVFNFRANQDPAISTPIYFPAANTEKARLLYETNP--LSFLS 183
Qy 178 PCVISEAGFYTVGKQDTPVOCFSCGGLKEMOBDPLDHTPCFPCNCFPLONMSSAEVTP 237
Db 184 PAKLAKAGFYIIGPGRDVACFACDGLKLSMERKDDAMSEHQRHFPSCFPLDLOQS----- 239
Qy 238 QYISYKGFVDITIGEHVSWVORELPMASAYCNDSI--FAYELRLDSFKWMPRESAVGV 296
Db 240 -----ASRYTVSNLSMOTHSARLRFLYMPSPVPV 278
Qy 297 ALAKAGLFTYGIKDIYOCFSCGGLKEMOBDPLDHTPCFPCNCFPLONMSSAEVTP 356
Db 272 QELASAGFYTVGSHSDVAKFCFCCDGLRCWESGDDPWVHAHAKWPFRCFELRMGO--EF 337
Qy 357 DLQSRGEICELLETTESNLEDSTAVGPIYVEMAOEACQFOEAKNLNFOILMAATS 413
Db 332 VOAGVPHLEQLLSTSDSP--EDENADAIVHFGESSESDVYMMSTPVYKALEMGFSRS 390
Qy 401 ---KNLNEQLRAA---YTSASFHMSLIDISSDL-----ATDHLGCDLSIAKHSK 447
Db 391 LVQTVORQIATGEBNYRTVSDIYIGLLADEDEKREOMQAAEEESDILLIRKNKV 450
Qy 448 PVQF-PLVLPVEFGNLNSVMCVGEAGSGKTYLKKIAFLMASGCCPLNRFOLYFVLSL 506
Db 451 LEQHLTCVTPYLTYCLLARAITDEECNAVY----- 480
Qy 507 SSTPRDGLASITCDQLLEKGSVTETCMRNITIOOLKNQV---LELDDYK-----EICS 558
Db 481 --QKPHLOASTLIDVYLA-KGNTAATSPRNSLRREIDPALYNDIVQODIRSLPTDIAA 537
Qy 559 IP--QVIGKLIQKHLNRCL 577
Db 538 LPMEQLRLK-GERMKYKCM 557

RESULT 11
BIR2_HUMAN
AC 013489; Q16628; Q9UP46; STANDARD; PRT; 604 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis

```

DE protein 1) (H1AP1) (H1AP2) (TNFR2-TRAF signaling complex  
 DE protein 1) (IAP homolog C).  
 GN BIRC2 OR API1 OR IAP1 OR MHC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 ON NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=66128127; PubMed=8548810;  
 RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related  
 RT to baculoviral inhibitor of apoptosis proteins.";  
 RL Cell 83:1243-1252(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96149249; PubMed=8552191;  
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertnon-Horvat G.,  
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
 RT family of IAP genes.";  
 RL Nature 379:349-353(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal Liver;  
 RX MEDLINE=96209843; PubMed=8643514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
 RT "Cloning and expression of apoptosis inhibitory protein homologs that  
 RT function to inhibit apoptosis and/or bind tumor necrosis factor  
 RT receptor-associated factors.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99252096; PubMed=10233894;  
 RA Horrevoets A.J., Pontijn R.D., van Zonneveld A.J., de Vries C.J.,  
 RA ten Cate J.W., Pannekoek H.;  
 RT "Vascular endothelial genes that are responsive to tumor necrosis  
 RT factor-alpha in vitro are expressed in atherosclerotic lesions,  
 RT including inhibitor of apoptosis protein-1, stannin, and two novel  
 RT genes.";  
 RL Blood 93:3418-3431(1999).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HEMEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN  
 CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,  
 CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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 CC -----  
 CC EMBL: LA9432; AAC41943.1; -  
 CC EMBL: U45878; AAC50371.1; -  
 CC EMBL: U37546; AAC50507.1; -  
 CC EMBL: AF070674; AAC83232.1; -  
 CC HSSP: Q13490; 10BH.  
 CC MIM: 601712; -  
 CC InterPro: IPR001370; BIR.  
 CC InterPro: IPR001315; CARD.  
 CC InterPro: IPR001841; znf\_fing.  
 CC Pfam: PF00653; BIR; 3.

DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR PROSITE: PS00518; zf\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS50089; zf\_RING\_2; 1.  
 KW Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 29  
 FT REPEAT 169  
 FT REPEAT 255  
 FT REPEAT 439  
 FT DOMAIN 557  
 FT ZN\_FING 592  
 FT CONFLICT 18  
 FT CONFLICT 119  
 FT CONFLICT 153  
 FT CONFLICT 163  
 FT CONFLICT 165  
 FT CONFLICT 191  
 FT CONFLICT 364  
 FT CONFLICT 552  
 FT CONFLICT 552  
 SQ SEQUENCE 604 AA; 68371 MW; 8581A0B9A9ABA47 CRC64;  
 Query Match 6.0%; Score 436.5; DB 1; Length 604;  
 Best Local Similarity 24.5%; Pred. No. 1.3e-18;  
 Matches 147; Conservative 84; Mismatches 200; Indels 169; Gaps 22;  
 QY 69 TYPEPSSWIP---QEMAAAGFYFTGVKSGICQFCGSLIFAGLTRLPIEDHKRPHPCG 125  
 DB 35 TYSTFPAGVPVSEKSLAAGFYTGVDKVCFCGGLMDMKRGDSPTKXKRLYPSCR 94  
 QY 126 FLIN-KDVGNT-----AKYDRVKNLKSRLRGK----- 153  
 DB 95 FVQSLNSVNNLEATSQPFPPSSVYNSTHSLPGLTENSQYFPGSYNSNSPNVNSRANDF 154  
 QY 154 ---NR-----YQEEARLASFRMPPFYVGQISPCVISEAGFYFTGKQDITYQCSGGCL 204  
 DB 155 SALNKSSYHCAMNNENALTFQTPW--LTFSLPDLAKAGFYIYIGPDRAVACFACGCKL 212  
 QY 205 GNMWEGDDPMKWKMPKCFELSKSKSEETIOTIOSYKGFVDITGHEFVNSWQRELTP 264  
 DB 213 SNMEPKDNAMEHLRHFKCFPIEMQ--LQDTSRTYS-----NLS 251  
 QY 265 MASAYCNDISIFAYEELRLDSFKDMPRESAVGVAAALAKAGLYFTGIKIDYQCSGGCL 324  
 DB 252 MOT-----HAARKTFEFPNPSVLYNPEDLASAGFYVGNSDYKCFCCDGGRLC 301  
 QY 325 WQGGDPLDDHTRCFPNCPFLQNMKSSAEVTPDLOSRCGLCELLTETSES----- 374  
 DB 302 WESGDDPMVQWAKMFRPCEYLRIKGEFIRQVQASYPHLLLEQLSTSDSGDENAESSI 361  
 QY 375 -----NLDSIAVYG-PIVEMAGQEAQWQKAKNLEOLBRAVYASPRHNSLIDIS 425  
 DB 362 IHPEPGEHSDALIMNTPTV--NAAVEMGFSRLVQYVOKRLIATEENR-----LV 413  
 QY 426 SDLATDHLGLCDLSIAKHSKIPQOEPLVLPVEFGNLNSVACVEGEASGTVLLKRIAF 485  
 DB 414 NDLYVID-LINMDETREREERATE-----EKESNDLLLRK-- 449  
 QY 486 LMASGCCPLNRPLVFLYLSLSTRPDEGL-ASIIQDQ-----LLEK- 526  
 DB 450 -----NRMLFQHLTCTVPIPLDSILTAGIINEQEHVIRKQTSIQAARELDIPTI 499  
 QY 527 --EGSVTECMKRNIIQOKL---NOVLPFLDDPK-----EISIPQVIGKLIQKNHLSPTC 576  
 DB 500 LKGNIAATVFRNSLQEAVALYELHFLVQODIKIYPTEDVSDLP--VEQLRRLQAEERTC 557

RESULT 12

BIR4\_MOUSE  
 ID BIR4\_MOUSE STANDARD: PRT: 496 AA.  
 AC 060989: 008865;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)  
 DE (IAP homolog A) (MIAP3) (MIAP-3).  
 GN BIR4 OR API3 OR XIAP OR AIPA OR MIPA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6 X CBA; TISSUE=Liver;  
 RX MEDLINE=96209843; PubMed=8643514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
 RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Parahant R., Lefebvre C., Korneluk R.G., McKenzie A.E.;  
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND CASPASE-7 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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 CC -----  
 CC EMBL: U36842; AAC52594.1; -;  
 CC EMBL: U88990; AAB58376.1; -;  
 CC HSSP: Q13490; 10BH.  
 CC MGD: MGI:107572; Birc4.  
 CC DR InterPro: IPR001370; BIR.  
 CC DR InterPro: IPR001841; Znf\_fing.  
 CC DR Pfam: PF00653; BIR\_3.  
 CC DR SMART: SM00238; BIR\_3.  
 CC DR SMART: PS01282; BIR\_REPEAT\_1; 3.  
 CC DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 CC DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 CC DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 CC KW Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 26 93  
 FT REPEAT 163 230 BIR 1.  
 FT REPEAT 264 329 BIR 2.  
 FT ZN\_FING 449 484 BIR 3.  
 FT CONFLICT 208 208 RING-TYPE.  
 FT CONFLICT 317 317 E -> K (IN REF. 2).  
 FT CONFLICT 322 322 W -> D (IN REF. 2).  
 FT CONFLICT 346 346 S -> C (IN REF. 2).  
 FT CONFLICT 360 360 S -> P (IN REF. 2).  
 FT CONFLICT 388 388 I -> L (IN REF. 2).  
 FT CONFLICT 449 449 C -> S (IN REF. 2).  
 FT CONFLICT 462 462 V -> F (IN REF. 2).  
 FT CONFLICT 468 468 V -> A (IN REF. 2).  
 FT CONFLICT 490 490 K -> N (IN REF. 2).  
 SQ SEQUENCE 496 AA: 56079 MW: EC5FAE07999F2CDD8 CRC64:

Query Match 5.9%; Score 431.5; DB 1; Length 496;  
 Best Local Similarity 28.8%; Pred. No. 2e-18;  
 Matches 121; Conservative 57; Mismatches 163; Indels 79; Gaps 12;  
 QY 60 EAKRLKTVTVTEPSSNTPDQMAAGFTYGVNSGIGCCFCSLILPGAGLTRLPID---- 116  
 DB 26 EFNRLKTPANPSSSPVASTLARAGFLYEGEDDVQCFSC-----AIDRQVGDNAV 80  
 QY 117 --HRRFPDC---GFLINDVGNIAKYDIRVANKSR----- 148  
 DB 81 GRHRRISPNCRFINGFYFENGAGQSTNPGLNQYKSENCVGNRPFADRPETHADYL 140  
 QY 149 LRGKMM-----RQEEARLASFRRMPFYVQGISPCVLSSEAGFVETGRQDTPVO 196  
 DB 141 LRTGQVYDIDDTTPRNPANCSEARLKSFOVMPDYAH-LTRRELASGLVYTGADDDVQ 199  
 QY 197 GFSGGCGCLNMEDGDDPKWEHAKWPKCEFLSKSSSEITQYIYSGVYDITGEHFN 256  
 DB 200 CFCCGCGKLEWMEPCDRAMSEHRRHPNCFVLCRN-----VNVRSSEGS 244  
 QY 257 SWQRELPMAAYCNDISFAYEELRDSFKDMPRESAVGVALAKAGLFTYGIQDVOCF 316  
 DB 245 S--DRNFPNSTSPNRPMAEYEAETVETGW--TSSVNRQLARAGFYALGEGDKYCF 300  
 QY 317 SCGGCLEKKQESDDPLDHTTRCFNCPFLONKSSAEVTPDLOSRGELCELLETSE--- 373  
 DB 301 HCGGGLTQKPEDEWQHAKWYPCGKYLDEKQ-EYNNIHILHSLSELSLGTAKTP 359  
 QY 374 ---SNLEDSIAVGPVPPMAGGEQWQEAKNLEQLPAATVSFRHMSLIDISSLAT 430  
 DB 360 SLTKRIDTITQNPVQALIMGFSFDIKTKMEKIOTSGSS---YLSLEVLIADLV 415  
 RESULT 13  
 BIR4\_RAT  
 ID BIR4\_RAT STANDARD: PRT: 496 AA.  
 AC 09R016;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)  
 DE (IAP homolog A) (RIAP3) (RIAP-3).  
 GN BIR4 OR API3 OR XIAP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Salto N.;  
 RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA";  
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND CASPASE-7 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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 CC -----  
 CC EMBL: AB033366; BAA85504.1; -;  
 CC HSSP: Q13490; 10BH.  
 CC DR InterPro: IPR001370; BIR.  
 CC DR InterPro: IPR001841; Znf\_fing.



DR Pfam; PF00653; BIR. 3.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR. 3.  
 DR SMART; SM00184; RING. 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS00518; zf\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; zf\_RING\_2; 1.  
 KW Apoptosis; zinc-finger; Repeat.  
 FT REPEAT 26 93 BIR 1.  
 FT REPEAT 163 230 BIR 2.  
 FT REPEAT 264 329 BIR 3.  
 FT ZN\_FING 449 484 RING-TYPE.  
 SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461AA69 CRC64;

Query Match 5.7%; Score 416.5; DB 1; Length 496;  
 Best Local Similarity 28.3%; Pred. No. 1.5e-17;  
 Matches 119; Conservative 60; Mismatches 162; Indels 79; Gaps 12;

QY 60 EAKRLKFTVYEPYSSWIPQMAAGFYFTGKSGICFCSCSLIFGAGLTRLPDIED--- 116  
 DB 26 EFNRLKFTFANPPSSPVASFLARAGFLYTGEGDTCVCFSCCH-----AAVDRMQYGSAY 80  
 QY 117 --HRRFPDGCFL-----LNKDVGNIAKYD 139  
 DB 81 GRHRISPNCRFINGFYFENGATGOSTSPGIONGQYKSCNCGNNHFLALDRPETHADYL 140  
 QY 140 IR---VNLKSLRLGKMKRROEERARLASFRNPFYVOGISPCVLSAGFYFTKQDTVQ 196  
 DB 141 LRTQVVDISTPTIYPRNPAMCSEARLKTFOGMPDYAH-LSPRELASAGLYTGTIDQVQ 199  
 QY 197 CFSCGGCLGWNEEDDDPMKEHAKWPKCEFLRSKSSSEIQTQYKGFVDINGEHNV 256  
 DB 200 CFCCGGCLGWNEEDDDPMKEHAKWPKCEFLRSKSSSEIQTQYKGFVDINGEHNV 244  
 QY 257 SWVQRELPMASAYCNDISFAYEELRLDSFKDMPRESAVGVAALAKAGLYTGIRDIYOCF 316  
 DB 245 S--DRNPNSTNSPRNPAMAEYDARIYVFCGW--LYSVNKGQLARAGFYALGEDDKVCF 300  
 QY 317 SCGGCLEKMGQDPLDDHTRCFPCNCPFLQMKSSAEVTPDLOSREGELCETLTTSE--- 373  
 DB 301 HCGGGCLTDMKPEBDPMWEDHAKWPGCYKYLDEKGO-EVINNIHRLTHSGESVPTAETKP 359  
 QY 374 ---SNLEDSIAVGPITYPEMAGSEAGQWEAKNLNQLRAATSAFRMSTLSDIAT 430  
 DB 360 SVTKKIDDTIFQNPWQVDEALMGFNFDIKTKMEKIQ---TSGS-NYLSLEVLADLV 415

## RESULT 14

BIR4\_HUMAN STANDARD; PRT; 497 AA.  
 AC P98170; Q9N014;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)  
 DE (IAP-like protein) (HILP)  
 GN BIR4 OR AP13 OR IAP3 OR XIAP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal heart;  
 RX MEDLINE=96149249; PubMed=8552191;  
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertnon-Horvat G., Faresani R., Mclean M., Ikeda J., Mackenzie A., Korneluk R.G., "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";  
 RT Nature 379:349-353(1996).  
 RL

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal heart;  
 RX MEDLINE=96256286; PubMed=8654366;  
 RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., RA Giffillan M.C., Shields H., Hardwick J.M., Thompson C.B.;  
 RT "A conserved family of cellular genes related to the baculovirus IAP RT gene and encoding apoptosis inhibitors.";  
 RL EMBO J. 15:2685-2694(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Graham D.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP FUNCTION  
 RX MEDLINE=97373959; PubMed=9230442;  
 RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;  
 RT "X-linked IAP is a direct inhibitor of cell-death proteases.";  
 RL Nature 388:300-304(1997).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND CASPASE-7.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: UBIDOTIOUS, EXCEPT PERIPHERAL BLOOD LEUKOCYTES.  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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 CC  
 DR EMBL; U45880; AAC50373.1; -;  
 DR EMBL; U32974; AAC50518.1; -;  
 DR EMBL; AL121601; CAB95312.1; -;  
 DR HSSP; Q13490; 10BH.  
 DR MIM; 300079; -;  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001841; znf\_fing.  
 DR Pfam; PF00653; BIR. 3.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR. 3.  
 DR SMART; SM00184; RING. 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS00518; zf\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; zf\_RING\_2; 1.  
 KW Apoptosis; zinc-finger; Repeat; Thiol protease inhibitor.  
 FT REPEAT 26 93 BIR 1.  
 FT REPEAT 163 230 BIR 2.  
 FT REPEAT 265 330 BIR 3.  
 FT ZN\_FING 450 485 RING-TYPE.  
 FT CONFLICT 162 162 S->C (IN REF. 1).  
 FT CONFLICT 423 423 Q->P (IN REF. 2).  
 SQ SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;

Query Match 5.6%; Score 407; DB 1; Length 497;  
 Best Local Similarity 30.0%; Pred. No. 5.7e-17;  
 Matches 124; Conservative 59; Mismatches 152; Indels 78; Gaps 19;

QY 60 EAKRLKFTVYEPYSSWIPQMAAGFYFTGKSGICFCSCSLIFGAGLTRLPDIED--- 116  
 DB 26 EFNRLKFTFANPPSSPVASFLARAGFLYTGEGDTCVCFSCCH-----AAVDRMQYGSAY 80  
 QY 117 --HRRFPDGCFL-----LNKDVGNIAKYD 139  
 DB 81 GRHRISPNCRFINGFYFENGATGOSTSPGIONGQYKSCNCGNNHFLALDRPETHADYL 140

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QY 149 LRGM-----RYOEEARLASFRNPFYVGISPCVLSAGVFRTKODTVO 196
DB 141 LRTOGVDSITIVPRNPAMYSSEARLKSFOIMPDIYAH-LTPRELLASAGLYYIGIDVOY 199
QY 197 CFSCGGCGGMMEEGDDPWKEIAKMFPCFELRSKSSSEITIOYOSKGFVDITGEHPN 256
DB 200 CFCCGGGALKMNEPCDRAMSEHRHFPNCFVLCRLN-----IRESDAVS-SDNFPN 252
QY 257 SWORELPMASAYCNDSTFAVEELRLDSFKOMPRESAVGAALAKGLFYTGIDIVOCF 316
DB 253 S---TNLPR-----NPSMADY-EARIFFTGTW--IYSVKEOLARAGFYALGEGKVCF 301
QY 317 SCGGCCEKMOEGDDPLDDHTRCFNCPQLONKSSAEVTPDLOSGELCELLETTSSES-- 374
DB 302 HCGGGLTDMKPSDDPWEOHAKMPPGCKYLLDQKGQ-EYINNIHLHSLSECLVTRTEKTP 360
QY 375 ----NLEDIAVGPVPE-MAOGEAOMFOEAKNLNDOLAAATSAFRIHMSLL 422
DB 361 SLTRRIDTIFQNPVQEAIRMGFS--FRDIKIMEE-KIQISGSNYSKLEVL 410

RESULT 15
BIR_CHICK
ID BIR_CHICK STANDARD: PRT: 611 AA.
AC Q90660:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis
protein).
GN ITA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OX NCBI_TaxID=9031;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RX MEDLINE=9710112; PubMed=8945639;
RA Digby M.R., Kimpleton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homologue of IAP that is expressed in T
RL lymphocytes."
CC 1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC 1- CELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC 1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC 1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC 1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC 1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC 1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC 1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR HSSP: Q13466; AAB48118.1;
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.

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DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE: PS0089; zf_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.
FT REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 446 536 CARD.
FT ZNFING 564 599 CARD.
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CAC64;

Query Match
Best Local Similarity 5.3%; Score 388; DB 1; Length 611;
Matches 142; Conservative 86; Mismatches 207; Indels 184; Gaps 21;

QY 60 EAKRLKFTVYEPYSSMIFQEMAAAGFYFTGKSGIOGFCGSLIFGAGLTRLPIDHR 119
DB 30 ELYRMSTFTFPVNPVNSRRLARAGFYITGVQKVCFCGLYLDNMPGDNAMEKHKO 89
QY 120 FHPDGGFLN-----KDVGN----- 135
DB 90 VYPSCFYQNMLSLNNLGLSTHSAFSPVANSLSLRSMTLSPEFQGVGFSGSSFP 149
QY 136 -----AKYDIRVKNLSRLRGKRYQEEARLASFRNPFYVGISPCVLSAGVF 188
DB 150 RDPVTTBRAEDL--SHLSKSLQNPMS--STEAKRLRTSHAMP--LMCLMPAEVAKALD 203
QY 189 TGKQOTVQFCSCGGLGWEEDDPPMKHAKMFPKCEFLSKSSSEITIOYOSKGFVD 248
DB 204 LGTAKVACVNCVGKLSMWEKPDNAMESHRHFPNCFVEN----- 244
QY 249 ITGEHFNVSQVQRELPMASAYCNDSTFAVEELRLDSFKOMPRESAVGAALAKGLFYTG 308
DB 245 -----LMRDP--SFVNSVNTQTHAKKFTINPTIPVQPEQLADAGFYVG 292
QY 309 IKDIVOCFCSCGCGLEKNOEGDDPLDDHTRCFNCPQLONKSSAEVTPDLOSR-----G 362
DB 293 RNDVKKCFCCDGGGLRCWESDDPWIEHAKMFPKCEYLIRYK--GGEFVSQVQAFPHLWN 351
QY 363 ELCELLETTSNLEDIAVGPVPEMAOGEAOMFOEAKNLNDOLAAATSAF----- 416
DB 352 SSC-----TSDKPYDEN--MDPII-HPEGESP-SEDAIMANTPVVKAALENGFSRRLIK 403
QY 417 -----RMSLIDSSDLAT-----DHLLGCDLSIAKHSKIPVO 450
DB 404 QTVOSKLTAEENYKTVNDVLSLTAEDKEKEKEKQFEVVASDDLSLIRN----- 457
QY 451 EPLVLEVEFGNLNSVACVEGEGSGK-----TVLIKIAF 485
DB 458 -----RMALFORLTVSPLIGLSLSAKVITELEHDVIAKOTTPQPSARELIDVTKGNA 513
QY 486 LMASGCCPLINRFQVLYSLSTR-----PDEGLASITCDILEK--EGSVTECMKNI 538
DB 514 ASIFRNC--LKQFDPLYLDLFEKSKMYVPTEVDSGLPMEOGLRLQDEETKVCADKE 571
QY 539 IODLKNOVFLDLDYKEIC 557
DB 572 V-----SIVFICGHLVYC 585

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Search completed: September 30, 2002, 15:07:03  
Job time: 184 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 30, 2002, 15:01:49 : Search time 31.33 Seconds  
(without alignments)  
4303.011 Million cell updates/sec

Title: US-09-830-338-1

Sequence: 1 MATOOKASDERISQFDHNL.....SKYLTILOKWLIPSPITQK 1403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR\_71:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6373.5	87.2	1232	2	A55478	neuronal apoptosis
2	4919	67.3	1447	2	T42628	neuronal apoptosis
3	462	6.3	618	2	S68450	apoptosis inhibito
4	431.5	5.9	604	2	S68449	apoptosis inhibito
5	407	5.6	497	2	S69544	apoptosis inhibito
6	345.5	4.7	497	2	S69545	apoptosis inhibito
7	332	4.5	496	2	S68452	apoptosis inhibito
8	326	4.5	358	2	JC5964	apoptosis inhibito
9	303.5	4.2	275	2	A45679	inhibitor-of-apopt
10	293.5	4.0	268	2	T10304	inhibitor of apopt
11	293.5	4.0	268	2	A53989	apoptosis-inhibiti
12	242.5	3.3	298	2	JC7568	kidney inhibitor o
13	241	3.3	1215	2	H84513	probable disease r
14	198	2.7	1192	2	T17255	hypothetical prote
15	194.5	2.7	997	2	T43523	protein kinase VPS
16	192	2.6	1454	2	S48264	disease resistance
17	181	2.5	1304	2	G85188	disease resistance
18	180.5	2.5	1041	2	C85189	disease resistance
19	178.5	2.4	1152	2	T31911	hypothetical prote
20	178.5	2.4	1317	2	B85189	disease resistance
21	177	2.4	1184	2	H71436	hypothetical prote
22	177	2.4	1294	2	T18546	flax rust resistanc
23	177	2.4	1301	2	D85188	apoptosis-inhibiti
24	175.5	2.4	275	2	T10310	conserved hypotnet
25	175	2.4	1830	2	E82909	disease resistance
26	175	2.4	1895	2	T06609	probable resistance
27	175	2.4	2467	2	D71437	root-knot nematode
28	168.5	2.3	1257	2	T06269	IAP1 orf27 - Bomby
29	168	2.3	292	2	T41772	

30	167.5	2.3	1837	2	T41023	probable nuclear p
31	167	2.3	4540	2	T30838	cytoplasmic dynein
32	165.5	2.3	286	2	D36828	orf13 protein - Au
33	165.5	2.3	1253	2	T45787	disease resistance
34	164.5	2.3	1134	1	A29944	chaoptin precursor
35	162.5	2.2	1590	2	B86398	protein T7N9.24 [1
36	162.5	2.2	2335	2	T40186	probable phosphat
37	161	2.2	789	2	T52067	hypothetical prote
38	161	2.2	1110	2	F84547	probable disease r
39	160	2.2	150	2	T28409	ORF MSV248 probabl
40	160	2.2	919	2	T05746	hypothetical prote
41	159.5	2.2	624	2	T28423	ORF MSV261 leucine
42	159	2.2	1019	2	C96519	probable disease r
43	159	2.2	1802	2	T00020	bacterial blight-r
44	159	2.2	4639	1	A54794	dynein heavy chain
45	159	2.2	4717	2	T41581	hypothetical coile

ALIGNMENTS

RESULT 1  
A55478  
neuronal apoptosis inhibitory protein - human  
N:Alternate names: NAIP  
C:Species: Homo sapiens (hmn)  
C>Date: 05-Jan-1996 #sequence, revision 05-Jan-1996 #text, change 02-Feb-2001  
C:Accession: A55478  
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yareghli, Z.; Farahani, R.; Balid  
d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.  
Cell 80, 167-178, 1995  
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in 1  
A:Reference number: A55478; M01D:95112344  
A:Accession: A55478  
A:Molecule type: mRNA  
A:Residues: 1-1232 <ROY>  
A:Cross-references: GB:U19251  
C:Genetics:  
A:Gene: GDB:SMA6; SMA  
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300  
A:Map position: Sq12.2-Sq13  
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane P  
F:94-110/Domain: transmembrane #status predicted <TM1>  
F:470-477/Region: nucleotide-binding motif A (P-loop)  
F:479-486/Domain: transmembrane #status predicted <TM2>  
F:476/Binding site: ATP (Lys) #status predicted  
F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.2% Score 6373.5 DB 2 Length 1232  
Best Local Similarity 95.9% Pred. No. 0  
Matches 1229 Conservative 1 Mismatches 1 Indels 51 Gaps 1

Qy	1	MATOOKASDERISQFDHNLPELSALGLDAVOLAKLEEBEORERAKMQGYNSOMSE	60
Db	1	MATOOKASDERISQFDHNLPELSALGLDAVOLAKLEEBEORERAKMQGYNSOMSE	60
Qy	61	AKRLKTFVTEPYSSWIRQEMAAAGFTYGVKSGIQCCCSLLFGAGLTRLPEDHRRF	120
Db	61	AKRLKTFVTEPYSSWIRQEMAAAGFTYGVKSGIQCCCSLLFGAGLTRLPEDHRRF	120
Qy	121	HPDCGFLNKDVGNIAKVDIVKLNLSRLRGKMYOEERLASFRRMPPYVGISPCV	180
Db	121	HPDCGFLNKDVGNIAKVDIVKLNLSRLRGKMYOEERLASFRRMPPYVGISPCV	180
Qy	181	LSEAGFVFTGRQDPTVOCFSCGCGCLGNMEGDDPMKEHAKMPKCEFLRSKSSSEITQYI	240
Db	181	LSEAGFVFTGRQDPTVOCFSCGCGCLGNMEGDDPMKEHAKMPKCEFLRSKSSSEITQYI	240
Qy	241	QSYKGFVDITGEHFNYSWVQRELPMASAYCNDISFAIEELRLDSFKDMPRESAVGVALA	300
Db	241	QSYKGFVDITGEHFNYSWVQRELPMASAYCNDISFAIEELRLDSFKDMPRESAVGVALA	300

```

QY 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDLS 360
Db 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDLS 360
QY 361 RGELECELETTESNLEDSIAVGPVPEMAQGEAOMFEAANLEDOURAATSAFRHMS 420
Db 361 RGELECELETTESNLEDSIAVGPVPEMAQGEAOMFEAANLEDOURAATSAFRHMS 420
QY 421 LDISSDATDHLGCGDLSIAKSHISKPQEPVLPEVFGNLSVMKVEGASGKTVLL 480
Db 421 LDISSDATDHLGCGDLSIAKSHISKPQEPVLPEVFGNLSVMKVEGASGKTVLL 480
QY 481 KKAIFLMAAGCCPLNRPQVLEYLSSTRDEGLASIIDOLEKRGVTEMKRNITQ 540
Db 481 KKAIFLMAAGCCPLNRPQVLEYLSSTRDEGLASIIDOLEKRGVTEMKRNITQ 540
QY 541 QLKNOVLFLLDDYKEICSIPOVIGKLIQKNHLSRTCLLIIVRTNRARDIRRYLETILEIQ 600
Db 541 QLKNOVLFLLDDYKEICSIPOVIGKLIQKNHLSRTCLLIIVRTNRARDIRRYLETILEIQ 600
QY 601 AFPPYNTVCILRLKFSHNMTLRKRFMYGKGNOSLOKIQKTPLEVAICAHMFOYPRDPS 660
Db 601 AFPPYNTVCILRLKFSHNMTLRKRFMYGKGNOSLOKIQKTPLEVAICAHMFOYPRDPS 660
QY 661 FDDVAVFKSTWERNLSLRNKATAEILKATVSCGELALKGFECCCFEPPNDLAEAGVED 720
Db 661 FDDVAVFKSTWERNLSLRNKATAEILKATVSCGELALKGFECCCFEPPNDLAEAGVED 720
QY 721 EDLTWCLMSKFTQRLRPYRFLSPAFQEFGLAGMLIELDSROEHODLGLYHLKQINS 780
Db 721 EDLTWCLMSKFTQRLRPYRFLSPAFQEFGLAGMLIELDSROEHODLGLYHLKQINS 780
QY 781 PMHTVATYNNFLNTVYSLPSTAGPKIVSHLHLVDNKESELENISENDYKHXOPEISLQ 840
Db 781 PMHTVATYNNFLNTVYSLPSTAGPKIVSHLHLVDNKESELENISENDYKHXOPEISLQ 840
QY 841 MOLLRLGMOICQAFVSNVSEHLVLAKTAYQSTVAAACSPVLAQFLQGRITLGLALNL 900
Db 841 MOLLRLGMOICQAFVSNVSEHLVLAKTAYQSTVAAACSPVLAQFLQGRITLGLALNL 900
QY 901 QYFPHPESSLILNSTRHPPIRKNKTSPPRAHPSVLETCFDSQOYPTIDODYASAFEPNME 960
Db 901 QYFPHPESSLILNSTRHPPIRKNKTSPPRAHPSVLETCFDSQOYPTIDODYASAFEPNME 960
QY 961 ERNLAEKEDNKSYMDOQRASPDLSGTWKLSPKQYKIPCLEVDVNDIDVYGOMLETL 1020
Db 961 ERNLAEKEDNKSYMDOQRASPDLSGTWKLSPKQYKIPCLEVDVNDIDVYGOMLETL 1020
QY 1021 MTVFSASQRIEHLNHSRGFIESTIRPALDELKASVTKCSISKLELSAAQOELLTLPSE 1080
Db 1021 MTVFSASQRIEHLNHSRGFIESTIRPALDELKASVTKCSISKLELSAAQOELLTLPSE 1080
QY 1081 SLEVSCTIQGODOIFPRLDQFLCKELSLVDLGNINVSFVDEEPPNFIHMEKLLIQISA 1140
Db 1081 SLEVSCTIQGODOIFPRLDQFLCKELSLVDLGNINVSFVDEEPPNFIHMEKLLIQISA 1140
QY 1141 EYDPSKLVKLIONSPLHWFHLKCNFFSDGSLMTMLVSCKKLTETIKRSDSFOAVPEVA 1200
Db 1141 EYDPSKLVKLIONSPLHWFHLKCNFFSDGSLMTMLVSCKKLTETIKRSDSFOAVPEVA 1200
QY 1201 SLPNFTSLKILNLEGOQFPDEETSEKFAVILGSLSNLEELLTPGDCGIYRAKLLIQOCC 1260
Db 1150 SLPNFTSLKILNLEGOQFPDEETSEKFAVILGSLSNLEELLTPGDCGIYRAKLLIQOCC 1260
QY 1261 QJHCLRVLSFFETLLNDSDVEI 1282
Db 1210 QJHCLRVLSFFETLLNDSDVEI 1231

```

RESULT 2  
 T42628  
 neuronal apoptosis inhibitory protein 2 - mouse  
 C:Species: Mus musculus (house mouse)

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C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T42628
R:Ratghgh, Z.; Dlez, E.; Gros, P.; MacKenzie, A.
Mamm. Genome 10, 761-763, 1999
A:Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for m
A:Reference number: 222179; MUID:99315342
A:Accession: T42628
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1447 <TAR>
A:Cross-references: EMBL:AF102871; NID:93860228; PID:93860229; PIDN:AAC73002.1
C:Genetics:
A:Gene: Naip2

Query Match      67.3%; Score 4919; DB 2; Length 1447;
Best Local Similarity 65.4%; Pred. No. 5e-301;
Matches 946; Conservative 180; Mismatches 277; Indels 44; Gaps 2;

QY 1 MATQOKASDERISQFQHNILPELALLGLDVAQVLAKELEBEOKERRAKQKQNSOMRSE 60
Db 1 MAOGEAVEELICEFPDDLVSELSTLRVDALSVLRQOEDDHKTRMKKQKGFNSQMRSE 60
QY 61 AKRLKFTVYTERYSNIPQEMAAAGFYFTGKSIQCFSCSILFLGAGTLPLTEDHKRF 120
Db 61 AKRLKFTVYTERYSNIPQEMAAAGFYFTGKSIQCFSCSILFLSTLRKLPLEHKKL 120
QY 121 HPDCGFLNKRQDNATKADYDIRVKNLSRLRGKMKYOEERARLASFRNRPYVGISPCV 180
Db 121 RECEPEFLKQDVNIGKIDIRKSPKEMLRGSKAYHEERARLSFPDMPFYAIGTSPRV 180
QY 181 LSEAGVFYFGKDDTYOCSCCGCGLANWEGDDPKWEKAKMFKCEFLRSKSSBEITQY 240
Db 181 LSAAGVFYFGKDDTYOCSCCGCGLANWEGDDPKWEKAKMFKCEFLRSKSSBEITQY 240
QY 241 OSYKGFVDITGEHFVNSVQRELPMASAYCNDISFAAEELRLDSFKDWPRESAVGAALA 300
Db 241 QSYEGFLVHTGEHFVNSVQRELPMASAYCNDISFAAEELRLDSFKDWPRESAVGAALA 300
QY 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDLS 360
Db 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDLS 360
QY 361 RGELECELETTESNLEDSIAVGPVPEMAQGEAOMFEAANLEDOURAATSAFRHMS 420
Db 361 RGELECELETTESNLEDSIAVGPVPEMAQGEAOMFEAANLEDOURAATSAFRHMS 420
QY 421 LDISSDATDHLGCGDLSIAKSHISKPQEPVLPEVFGNLSVMKVEGASGKTVLL 480
Db 421 LDISSDATDHLGCGDLSIAKSHISKPQEPVLPEVFGNLSVMKVEGASGKTVLL 480
QY 481 KKAIFLMAAGCCPLNRPQVLEYLSSTRDEGLASIIDOLEKRGVTEMKRNITQ 540
Db 481 KKAIFLMAAGCCPLNRPQVLEYLSSTRDEGLASIIDOLEKRGVTEMKRNITQ 540
QY 541 QLKNOVLFLLDDYKEICSIPOVIGKLIQKNHLSRTCLLIIVRTNRARDIRRYLETILEIQ 600
Db 541 QLKNOVLFLLDDYKEICSIPOVIGKLIQKNHLSRTCLLIIVRTNRARDIRRYLETILEIQ 600
QY 601 AFPPYNTVCILRLKFSHNMTLRKRFMYGKGNOSLOKIQKTPLEVAICAHMFOYPRDPS 660
Db 601 AFPPYNTVCILRLKFSHNMTLRKRFMYGKGNOSLOKIQKTPLEVAICAHMFOYPRDPS 660
QY 661 FDDVAVFKSTWERNLSLRNKATAEILKATVSCGELALKGFECCCFEPPNDLAEAGVED 720
Db 661 FDDVAVFKSTWERNLSLRNKATAEILKATVSCGELALKGFECCCFEPPNDLAEAGVED 720
QY 721 EDLTWCLMSKFTQRLRPYRFLSPAFQEFGLAGMLIELDSROEHODLGLYHLKQINS 780
Db 721 EDLTWCLMSKFTQRLRPYRFLSPAFQEFGLAGMLIELDSROEHODLGLYHLKQINS 780
QY 781 PMHTVATYNNFLNTVYSLPSTAGPKIVSHLHLVDNKESELENISENDYKHXOPEISLQ 840
Db 781 PMHTVATYNNFLNTVYSLPSTAGPKIVSHLHLVDNKESELENISENDYKHXOPEISLQ 840
QY 841 MOLLRLGMOICQAFVSNVSEHLVLAKTAYQSTVAAACSPVLAQFLQGRITLGLALNL 900
Db 841 MOLLRLGMOICQAFVSNVSEHLVLAKTAYQSTVAAACSPVLAQFLQGRITLGLALNL 900
QY 901 QYFPHPESSLILNSTRHPPIRKNKTSPPRAHPSVLETCFDSQOYPTIDODYASAFEPNME 960
Db 901 QYFPHPESSLILNSTRHPPIRKNKTSPPRAHPSVLETCFDSQOYPTIDODYASAFEPNME 960
QY 961 ERNLAEKEDNKSYMDOQRASPDLSGTWKLSPKQYKIPCLEVDVNDIDVYGOMLETL 1020
Db 961 ERNLAEKEDNKSYMDOQRASPDLSGTWKLSPKQYKIPCLEVDVNDIDVYGOMLETL 1020
QY 1021 MTVFSASQRIEHLNHSRGFIESTIRPALDELKASVTKCSISKLELSAAQOELLTLPSE 1080
Db 1021 MTVFSASQRIEHLNHSRGFIESTIRPALDELKASVTKCSISKLELSAAQOELLTLPSE 1080
QY 1081 SLEVSCTIQGODOIFPRLDQFLCKELSLVDLGNINVSFVDEEPPNFIHMEKLLIQISA 1140
Db 1081 SLEVSCTIQGODOIFPRLDQFLCKELSLVDLGNINVSFVDEEPPNFIHMEKLLIQISA 1140
QY 1141 EYDPSKLVKLIONSPLHWFHLKCNFFSDGSLMTMLVSCKKLTETIKRSDSFOAVPEVA 1200
Db 1141 EYDPSKLVKLIONSPLHWFHLKCNFFSDGSLMTMLVSCKKLTETIKRSDSFOAVPEVA 1200
QY 1201 SLPNFTSLKILNLEGOQFPDEETSEKFAVILGSLSNLEELLTPGDCGIYRAKLLIQOCC 1260
Db 1150 SLPNFTSLKILNLEGOQFPDEETSEKFAVILGSLSNLEELLTPGDCGIYRAKLLIQOCC 1260
QY 1261 QJHCLRVLSFFETLLNDSDVEI 1282
Db 1210 QJHCLRVLSFFETLLNDSDVEI 1231

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Db 35 TYSTPAGVPSVRSRLARAGFYTGVDNDKVKFCGGLMLDNMKRGDSPTKHKIKLYPSCR 94
QY 126 FLIN-KDVONI-----AKYDIRKN-LKSLR-----150
Db 95 PVQSLNSVNNLEATQPTFPSSVTHSHSLPGTENGFRGYSNPSNPVNSRANQEP 154
QY 151 GCKMR-----YQEEALASFRRMPFYVOGISPCVISEGAFVFTKOTVOCSCGGL 204
Db 155 SALMRSSTPCCNNNNENALTLFTQWP--LTFLESTDLARAGFYIIPGGRVACFACGGKL 212
QY 205 GMEGDDPMKHAKEPCKCEFLRSKSSSEITQYOSKGFVDITGEHFVNSVQREL 264
Db 213 SNMEKONAMSEHRLHPPKCPTENG--LQDTSRTVS-----NLS 251
QY 265 MASAYCNDISFAVEBELRLDSFKDMPRESAVGAALAKAGLFTGIDKIDVOCSCGGL 324
Db 252 MQT-----HAARFKTFEFPSSVLVNPQOLASAGFYVGSNDVYKFCGDDGLRC 301
QY 325 MOEGDDPLDHTRCFPNCPFLONKSSAEVTPDLSRGLCELLETTSSES-----374
Db 302 WESGDDPWQHAKEPCKCEFLRSKSSSEITQYOSKGFVDITGEHFVNSVQREL 361
QY 375 -----NLEDSIANG-PIVEMAQGFQNFQEAKNLEQRLAAVTSASFRHMSLDD 425
Db 362 IHLEPGEHSEDAIMNTPVI--NAVEMGFSRLVQVQRKILATGENYR-----443
QY 426 SDLATDHLIGDLSIAKHHSKPVQEPVLPVEVGNLSWCVGEGAGSKTYLAKIAF 485
Db 414 NDLVLD-LNMADELFREERERATE-----EKESNDLLIRK---449
QY 466 LMASCCPLNRFQVLFYLSLSTRPEGL-ASITCDQ-----LLEK- 526
Db 450 -----NRMALFQHLVCVPIILDLSLTAGIINQEHVDYIKQTOFSLQARELIDI 499
QY 537 --EGSVTEMCMRNITQOLK---NOVLELDDYK-----EICSIPQVICKLQKNHLSITC 576
Db 500 LVKGNIAATVFRNSLOBAEAVLYEHLFVQODIKYIPTEDVSLP--VEQLRLRPEBRTC 557

RESULT 5
569544
Apoptosis Inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; #68451
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, M.C.
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:CROSS-references: EMBL:U32974; NID:91016687; PIDN:ANC50518.1; PID:91016688
Relation, P.; Roy, N.; Tamai, K.; Lefevre, C.; Baird, S.; Chertion-Horvat, G.; Farhan,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A:CROSS-references: EMBL:U45880; NID:91184319; PIDN:ANC50373.1; PID:91184320
C:Genetics: 11P
C:Gene: 11P
C:Function: 11P
A:Description: apoptotic suppressor
C:Superfamily: Apoptosis Inhibitor IAP homolog; RING finger homology
C:Keywords: Apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

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Query Match 5.6%; Score 407; DB 2; Length 497;

Best Local Similarity 30.0%; Pred. No. 8.2e-18;

Matches 124; Conservative 59; Mismatches 152; Indels 78; Gaps 19;

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QY 60 EAKRLKTEVYEPYSSMIPQEMAAGFYTGKSGICFCCSLILFAGLRLPIED---116
Db 26 EFNRLKTFANFPGSPVSASTLARAGFLYTGEGDVRCSCH-----AAVDRMGYDSAV 80
QY 117 --HKRFPDPC-----GPLANKDY-----GNAKYDIRKN-LKSR-----148
Db 81 GHRKVSPPCRINQFNLNATSTQSTNGIQNGYKVENTLGRDHFALDRSETHADYL 140
QY 149 LRGCKM-----RYQEEARLASFRMPFYVOGISPCVISEGAFVFTGKODTVO 196
Db 141 LMTGQVVDISDTYPRNPAMTSEARLKSQNPDIH-LTPRELASAGLYTIGCDQV 199
QY 197 CFSCGCGKMGEGDDPMKHAKEPCKCEFLRSKSSSEITQYOSKGFVDITGEHFVN 256
Db 200 CFCCGCKLMKNEPCDRAHSEHRRHFPNCFVLCRLN-----IRSEDAVS-SDRNPN 252
QY 257 SWQRELPMASANCNDISFAVEBELRLDSFKDMPRESAVGAALAKAGLFTGIDVOCF 316
Db 253 S--TNLPR-----NPSMADY--EARIFETGW--IYSVAKDOLARAGFYALGEGDKYCF 301
QY 317 SCGCGCLEKMOEGDDPLDHTRCFPNCPFLONKSSAEVTPDLSRGLCELLETTSSES--374
Db 302 HCGGGLTDMKPSDEDPWEQHAKEPCKCKTYLLEQKQ-EYINNHLTHSLGCVLRTTEKTP 360
QY 375 ---NLEDSIANGVTYPE-MAQGAQNFQEAKNLEQRLAAVTSASFRHMSL 422
Db 361 SLTRRTDITFONPWQEAIRMGFS--FKDIKIMEE-KIOISGNKSLLEV 410

RESULT 6
569545
Apoptosis Inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan,
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286
A:Accession: S69545
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:CROSS-references: EMBL:U32373; NID:91019116; PIDN:ANC47155.1; PID:91019117
C:Genetics: 11P
C:Gene: 11P
C:Superfamily: Apoptosis Inhibitor IAP homolog; RING finger homology
F:446-490/Domain: RING finger homology <RRN>

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Query Match 4.7%; Score 345.5; DB 2; Length 497;

Best Local Similarity 26.2%; Pred. No. 6.1e-14;

Matches 114; Conservative 65; Mismatches 161; Indels 95; Gaps 16;

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QY 57 MRSEAKRLKTEVYEPYSSMIPQEMAAGFYTGKSGICFCCSLIL-----FGAG 108
Db 6 MELDSVRLATFGEPLNAPASABDLVANGFPATGNMLEBCHFCVDRIDRDEYQDVAVG 65
QY 109 LTRLPIEDHRRFHPDCCGFLNKNQ-VGNIKAYDIRKNLSRLRGKMKRYQEEA-----161
Db 66 -----HRRSPISCSMWLAPRHCGNV-----RSQESDNEGNSVYDSESCDCL 111
QY 162 ----PLASFRMPFYVOGISPCVISEGAFVFTGKODTVOQSCGCGKLMNEBGDDPMK 217
Db 112 LEANRLVYTRFDWP--NPNTTPOALAKAGFYTLNLDHAKCYWCKGVAKEKNDNAFEH 169
QY 218 AKWFKPC-----EFLRSKSSSEITQYOSKGFVDITGEHFVNSVQRELPMASA 268
Db 170 KRFPQCPRVQNGPLIEFRATGKNLDE-----LGIQPTT-----LPLRK 208

```



Db 65 KMAPQCFVNG-----IDVGSIVTNNIQ-----NTTHDTITIGA 101

Qy 275 ---FAVEELRLDSFKDMPRESAVGAALAKAGLEFYTGIDIVQCFSCGGCLGNMBEGDDP 331

Db 102 HKPAARLGTYYNMP--VQFLPSRMAASGFYILGRGDEVCAFCARCYEITNMVAGDDP 161

Qy 332 LDDHTCFPNCPLQNMKSSAEVTPDLSRGEICELL-ETTSSENLDSIAVGPYPE 368

Db 162 MEQHVHMFPRCAVQVLKGRDYYQKVT---EACVLPGEINTVST---AAPVSEPIPE 213

## RESULT 10

TI0304

Inhibitor of apoptosis protein 3 - Orygia pseudotsugata nuclear polyhedrosis virus

C:Species: Orygia pseudotsugata nuclear polyhedrosis virus, OpMPV

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 15-Sep-2000

C:Accession: TI0304

R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohmann, G.F.

Virology 229, 381-399, 1997

A:Title: The sequence of the Orygia pseudotsugata multineucleocapsid nuclear polyhedrosis

A:Reference number: 217011; MUID:97271300

A:Accession: TI0304

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-268 &lt;AHR&gt;

A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

F:217-261/Domain: RING finger homology &lt;RRN&gt;

## Query Match

Best Local Similarity 4.0%; Score 293.5; DB 2; Length 268;

Matches 68; Conservative 34; Mismatches 88; Indels 33; Gaps 6;

Qy 157 QEEELRLASFRNMPFYVQGISPCVLSAGFVFTGKODIVQCFSCGGCLGNMBEGDDP 216

Db 16 KMKARLGTYYNMP--VQFLPSRMAASGFYILGRGDEVCAFCARCYEITNMVAGDDP 73

Qy 217 HAKWPKCEFLRSKSSSEITQYIQSYKGFVDITGEHFNWSVQRELPMASAYCNDSTFA 276

Db 74 HKRMAPQCFVRNNAHDT-----PH-----DRAPPARSAAHPO-YA 109

Qy 277 YEELRLDSFKDMPRESAVGAALAKAGLEFYTGIDIVQCFSCGGCLGNMBEGDDP 336

Db 110 TEARLRTFAEMPRGLKORPEELAEAGFYTGQDTRCFCCDGLKMDPDDAPMQHA 169

Qy 337 RCFPNCPLQNMKSSAEVTPDLSR--GELCELETTSSNLE 377

Db 170 RWDRCREYVLLVGR-----DEVQRYMTEACVVRADNENPHIE 207

## RESULT 11

A53989

apoptosis-inhibiting protein - Orygia pseudotsugata multicapsid nuclear polyhedrosis virus

C:Species: Orygia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMPV

C:Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 15-Sep-2000

C:Accession: A53989

R:Binbaum, M.J.; Clem, R.J.; Miller, L.K.

J. Virol. 68, 2521-2528, 1994

A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polyh

A:Reference number: A53989; MUID:94187094

A:Accession: A53989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-268 &lt;BIR&gt;

A:Cross-references: GB:L22564; NID:g456111; PIDN:AAB02610.1; PID:g456114

A:Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as As

F:217-261/Domain: RING finger homology &lt;RRN&gt;

## Query Match

Best Local Similarity 4.0%; Score 293.5; DB 2; Length 268;

Matches 68; Conservative 34; Mismatches 88; Indels 33; Gaps 6;

Qy 157 QEEELRLASFRNMPFYVQGISPCVLSAGFVFTGKODIVQCFSCGGCLGNMBEGDDP 216

Db 16 KMKARLGTYYNMP--VQFLPSRMAASGFYILGRGDEVCAFCARCYEITNMVAGDDP 73

Qy 217 HAKWPKCEFLRSKSSSEITQYIQSYKGFVDITGEHFNWSVQRELPMASAYCNDSTFA 276

Db 74 HKRMAPQCFVRNNAHDT-----PH-----DRAPPARSAAHPO-YA 109

Matches 68; Conservative 34; Mismatches 88; Indels 33; Gaps 6;

Qy 157 QEEELRLASFRNMPFYVQGISPCVLSAGFVFTGKODIVQCFSCGGCLGNMBEGDDP 216

Db 16 KMKARLGTYYNMP--VQFLPSRMAASGFYILGRGDEVCAFCARCYEITNMVAGDDP 73

Qy 217 HAKWPKCEFLRSKSSSEITQYIQSYKGFVDITGEHFNWSVQRELPMASAYCNDSTFA 276

Db 74 HKRMAPQCFVRNNAHDT-----PH-----DRAPPARSAAHPO-YA 109

Qy 277 YEELRLDSFKDMPRESAVGAALAKAGLEFYTGIDIVQCFSCGGCLGNMBEGDDP 336

Db 110 TEARLRTFAEMPRGLKORPEELAEAGFYTGQDTRCFCCDGLKMDPDDAPMQHA 169

Qy 337 RCFPNCPLQNMKSSAEVTPDLSR--GELCELETTSSNLE 377

Db 170 RWDRCREYVLLVGR-----DEVQRYMTEACVVRADNENPHIE 207

## RESULT 12

JC7568

Kidney inhibitor of apoptosis protein - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C:Accession: JC7568

R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.

Biochem. Biophys. Res. Commun. 279, 820-831, 2000

A:Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.

A:Reference number: JC7568; MUID: 21092523

A:Contents: Fetal kidney

A:Accession: JC7568

A:Molecule type: mRNA

A:Residues: 1-298 &lt;LIN&gt;

A:Comment: This protein, a new member of the inhibitor of apoptosis protein family, p

C:Genetics:

A:Gene: KIAIP

A:Map position: 20q13.3

A:Keywords: apoptosis

Query Match

Best Local Similarity 3.3%; Score 242.5; DB 2; Length 298;

Matches 54; Conservative 15; Mismatches 44; Indels 11; Gaps 4;

Qy 159 EEARLASFRNMPFYVQGISPCVLSAGFVFTGKODIVQCFSCGGCLGNMBEGDDP 218

Db 87 EELRLASFRNMPFYVQGISPCVLSAGFVFTGKODIVQCFSCGGCLGNMBEGDDP 218

Qy 219 HAKWPKCEFLRSKSSSEITQYIQSYKGFVDITGEHFNWSVQRELPMASAYCNDSTFA 276

Db 146 KMFPCOFLRSKGRD-----FVHS-----VQETHSQLGSDMPDEEEDAPPAVAPSVFASG 197

Qy 277 YEEL 280

Db 198 YPEL 201

## RESULT 13

H84513

Probable disease resistance protein (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: H84513

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon,

Gus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: H84513

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 &lt;LIN&gt;



A:Residues: 1-1215 <STO>  
 A:Cross-references: GB:AE002093; MID:96598711; PIDN:AAD25848.2; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g14080  
 A:Map position: 2

Query Match 3.3%: Score 241; DB 2; Length 1215;  
 Best Local Similarity 19.8%; Pred. No. 8,9e-07;  
 Matches 226; Conservative 165; Mismatches 383; Indels 370; Gaps 52;

```

QY 368 LETTSNLEDSIAVGPVLPVEMAG-----EAGW----- 396
DB 84 IDFTDNNIERKSGIPGLIAIKSKIAYVLLSKDYASSWMCNLEVEIKKGRMLDQT 143
QY 397 ----FOE-----AKNLEOLRAAYTSASFRHMSLDDISSLDADHLICDLS 439
DB 144 VMTIFVEVDPTDYKQGGDFGVKVKTCMGTNAVSRRKIMALEVATIAGEHSIMDT 203
QY 440 IA-----SKHSKPVGEPLVPEVFG-----NLNSVQVE-----GEAGSG 475
DB 204 AAMTEKISTDJSNKLNNSTPLRDFDGLVGMCAHMEKLELLCLDSCEYRMIGWPGEG 263
QY 476 KTVLLKRIAFIMASGCCPLNRFQVLFY-----SLSTRPDEGLASIIDQLLEK-- 526
DB 264 KTTIVR---FLYNQ-----LSSSFELSTFMENIKMTHTLASDDYSAKLIQRQPLSKIL 316
QY 527 EGSVTECMRNIIQO--LKNQVLEFLDDYKEICSIPOYIGLIKQKHLSTRCLLIAYFTN 584
DB 317 DHKDEIPHLVLOERLYNKKVLVVDL-----VDQSVOLDALAKETRWFGPRS- 365
QY 585 RADIRRLRLEIKAFPPYNTVCILRKLFSSHMTLRKRFMYV--FGKNQSLQIKQTP- 642
DB 366 -----RLITTOQRKLKAHRINNIYKVDLPPSDDLQITCMYAFG-----OKTPY 411
QY 643 --LEVAICAHWF--QYPPDFSPDDAVAFKSYMERLSLRNKATAEI--LKATVSSCGELA 696
DB 412 DGFYKLARKVTLVGNFPL-----GLRVGSYFREM--KQEMRKEIPLRLARLDKIESV 465
QY 697 LKGFSCCFEENDDLAEGVDEDEDLTMCMSKFTAORLRFPRFLSPAQEFLAGRL 756
DB 466 LK-----FSYDALC---DEKDLFLHIACFNHESIKLEDFLKTPE----- 504
QY 757 IELDSRHOEHQDGLYHLKQINSRPMYTSAYNNFLNYSLSPTKAGPKIV----- 808
DB 505 ---LDIAQRH-----VLAEKSLISINSFVEMHDSL--AQLEKEIVKQSVAPR 549
QY 809 SHLHLVDNKESLENSENDYLRKQPEISLOMOLLRG--LMOICPOAYFSMVSEHLVL 866
DB 550 GORQFLVDARDISEVLA--DDTAGGRSVYIGIYLDLHRNDVFNISEKAFEGM--SNLOFL 605
QY 867 ALKRAYGSNTVAAACSPFYLOGLQRTLTGLALNLOYPFDHESLSLRSIHPIRGKNTS 926
DB 606 RVKNRGNLFPALVCIPLCLTYIS-----RKRLRLDMWYTFPM----- 641
QY 927 PRAHFSVLETCFDSQVFTIDQYASAPR-----MNEMERNLAEKEDNVASYMDMORA 981
DB 642 -----TGF-----PSKFNPELVELNMGSKLEKMEIOPPLRNLR-- 678
QY 982 SPDLSTGYWKLSPROYKIPCLEVDVNDIDVVGODMLIELMTVFSASQRIEHLNHSRGI 1041
DB 679 -----MDLFSKNLKLKELPPLSSATNTLEVNLNMGCSLTV 711
QY 1042 ESIRPALELSASTKSGISKLELSAABOEILLPLSLESLEVGSTIOSQOQIPNLDKF 1101
DB 712 E-----LPFSIGNATK--LTKLELSGCS--LLELP--SIGNAIVLQITDSHCNLT 758
QY 1102 L-----CLKEISVLEGNINVEFVPEEPFNHMEKL-LIQISAETDSKVLKL 1150
DB 759 VELSSIGNATNKLKELDSSCSL--KELPSSIGNCTNKLKHLICSS--LKELPSS 812
QY 1151 IONSPLNHLVFLKC-----NFFSPDGLMTM--LVSCKRLTEIKFSDFEQAVPFAVS 1201

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DB 813 IGNCNLKELHLTCCSSSLIKLPSSIGNAINTKELLIACGESLVE----- 856
QY 1202 LPNLF-----SUKTINTLEQOQRPDETSKFAVILGSLNLEEL-----ILPTGGGI 1248
DB 857 LPSPFGKATNKLKTLNLTGLYSLCLVELP--FTGNLKRISLELRGCKQLQVLEPTNLT 911
QY 1249 YRVAKLLIQOCCQHLCLVLSFFFTLNDSDVEIAKVAISG-----GFOKLENT 1297
DB 912 EFLNELDITDCLILKTFPVIS-----TNIKRHLRTOQLIEVPSSLSRSPRLLED 961
QY 1298 KLSINHKITEEGYRNFGQALDNMPNLOELDISRHETECIKAAQATVNSLSQCVLRPLI 1357
DB 962 QMLXSENLS-----FSVILRITVLELSDIN-----IREMTWMLNRITRLR 1003
QY 1358 RLNM 1361
DB 1004 RLKL 1007

```

## RESULT 14

T117255  
 hypothetical protein DKFZp58601822.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T117255  
 R:Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 Submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18722  
 A:Accession: T117255  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1197 <ROE>  
 A:Cross-references: EMBL:AL117470  
 A:Experimental source: adult uterus; clone DKFZp58601822  
 C:Genetics:  
 A:Note: DKFZp58601822.1

Query Match 2.7%: Score 198; DB 2; Length 1192;  
 Best Local Similarity 20.8%; Pred. No. 0.00044;  
 Matches 158; Conservative 108; Mismatches 282; Indels 212; Gaps 34;

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QY 450 QEPVY-----LPEVFG--NLNS-----VMCEGAGSGKTVLLKRIAFIM 487
DB 11 QDPLVKRSPROYVEENRGLHLEINDLFGPLDQEPRIYILOGAAGIKSTLQAQVKEAM 70
QY 488 ASGCCPLNRFQVLYSLSTRPDEGLASIIDQLLEKESVTECMRNITIQDLKNQVL 547
DB 71 GRGQL--YGDRLFQHVYFSGRELAQSK--VVSIAELIGKDGSTATPAPRIQLTSR--PERLL 125
QY 548 FLDDY-----KEIC--SIPO-----VIGKLIKQKHLSTRCLLIAYRTRNRADI 589
DB 126 FILDGVDEPGVLOEPSSSELCLHNSQPPADALGSLGKTLPEPASLITARTLAQNTL 185
QY 590 RRYLETI--LEIKAFPPYNTVCILRKLFSSHMTLRKRFMYVFGKNOSLOKIQKPTLFAVA 647
DB 186 IPSLEQAAWVEVLGFSSESREKRYPRITTDEROAIRARL--VKSKEKMAALCLPWPVSWL 244
QY 648 ICAMHFOYPPDFSPDDAVAFKSYMERLSLRNKAT-----AEIKATVSSCGE 694
DB 245 ACTCLMQO-----MKRREKLVTGSKTTTTLCLHYLAQALQAPGQPLRDICS 292
QY 695 LALKGFSCCFEENDDLAEGVDEDEDLTMCMSKFTAORLRFPRFLSPAQEFLAGM 754
DB 293 LAAGELWQKTLFSPDDLRKRGLDAAIISTFLKGLIOEHPIPLSYFIHLCPQEFPAAM 352
QY 755 RLIELDSRHOEHQDGLYHLKQINSRPMYTSAYNNFLNYSLSPTKAGPKIVSHLLHL 814
DB 353 SYVLEDEKGRKHSHNC-IIDLEK-----TLEAVG-----IHGL--FGASTRFLFLGL 396
QY 815 V--DNKESLENI-----SENDYLRKQPEISLOMO-----LLRGIMQICPOAYFSMVSEH 862
DB 397 LSEGEREMENIFHCRLSOGRNLMQWPVSLQILLQPHSLSLHCLYETRNRKTFLLQVMAH 456

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QY 863 L--LVALKTAYQSNVTAACSPF-----VLOFLOGRTLTLGALNLQYFEDHDESLSLRS 915  
 Db 457 FEEMGMCVETDMLLVTCTFCIKFSRNHYKALQITEGR-----QHSTSPIMV 503  
 QY 916 IHPIRGNKTSRPAHNSVLETCGDKSQVPTIDODYASAFENWENRNLAE-----K 967  
 Db 504 VLF-----RMVPTDAVMQILFSLV-KYTRNLKLELDSGNSLS 540  
 QY 968 EDNYSKSYMQRRA-----SPDLSTGYKLSKQYKIPCLEVDYNDI 1009  
 Db 541 HSAVSKSLCTLRPRCLLETLELRLAGGLTAECCKDLAFG---LRANQ-TLTELDELSPNVL 596  
 QY 1010 DVG-----ODMEILMTFVSASORI-ELHLNHS----- 1037  
 Db 597 TDGAHNLGRLORLQPSCKLQRLQVSCGLTSDCCDLASVLSASPSLKELDLQNNLDV 656  
 QY 1038 --RGFTESLR-PALELSKASVTKSIS---KLELSAAE 1071  
 Db 657 GYRLCEGLRHAPACKLRILGLDQTLTSDENQELRALEOE 636

## RESULT 15

T43523

cut17 protein - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Jun-2000  
 C:Accession: T43523; T41649; T41700  
 R:Motilata, J.; Matsusaka, T.; Yanagida, M.  
 submitted to the EMBL Data Library, August 1999  
 A:Description: Fission yeast cut17 is required for chromosome segregation.  
 A:Reference number: 222536  
 A:Accession: T43523  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-997 <MOR>  
 A:Cross-references: EMBL:AB031034; PIDN:BA83415.1  
 R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, August 1998  
 A:Reference number: 222007  
 A:Accession: T41649  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-997 <HAR>  
 A:Cross-references: EMBL:AL031323; PIDN:CAA20424.1; GSPDB:GN00068; SPDB:SPCC962.02c  
 R:Medler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, October 1999  
 A:Reference number: 222010  
 A:Accession: T41700  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 932-997 <MED>  
 A:Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10c  
 C:Genetics:  
 A:Gene: cut17; SPCC962.02c; SPDB:SPCP31B10.10c  
 A:Map position: 3L  
 A:Introns: 43/3

## Query Match

Best Local Similarity 2.7%; score 194.5; DB:2; Length 997;  
 Matches 232; Conservative 177; Mismatches 447; Indels 365; Gaps 60;

QY 147 SRLRGKMYRQEEEARLASF--RAMPFYVQGISPCVLSSEAGFVYT-----GKDDTVQ 196  
 Db 13 NRRRRMCMYK---RLDTFOKKWPRAKP--TPETLATVGFYNNPISSEENSEERLDNVT 67  
 QY 197 CSCGGCCGANNMEEDDPKPKHAKWPKCEPLRSKSSSELTQYIYQKGFVDITGEPVN 256  
 Db 68 CWCCKSFYDWEDEDDPLKEHITHSPSCPW-----AVILSSK-----N 105  
 QY 257 SWVQRELPMASAYCNDISFATFEELRDSFDKMDPRESAVGVALAKAGLGY---TGIKDLV 313

Db 106 NPANQPAALALRKCRQRTFVQKVPYTRNRPDYHCEPSV---MAASGFYVNPAPAKDA 161  
 QY 314 OCFSGGCCLEKQNEQDDPLDHTRCFPCPLQNMKSSAEVTPDLOSRGLCELETTSE 373  
 Db 162 RCLYCDINLHDEPPDDPYTEKRRRACVFF-TWKQPNLSLPKLS-----FLSTSN 213  
 QY 374 SNLEDSIAVGPVTPMAQGEAOWFOEAKNLEQLRAAYTSASFRHNSLDDISSDLATDHL 433  
 Db 214 IDPEDLTEDNSILPVSPTRDST--KSHKTLN-----FSPSRKNNNANRPLMSLYT 262  
 QY 434 LGCDLSIAKHSKIPVQ-----EPLVL-----PEVGNLSNWCVEGAG 473  
 Db 263 ---NTSEEDSOPTRAPQPTKPYLLTPRRKKNKSPKSKRAYKPKVPKPLFSDDEDD 317  
 QY 474 SGKTVLLKRIAFVMAAGCC-----PL-----NRQLVFYLSLSTRPDE 513  
 Db 318 DDLTA-----SOPFSKICDMSQVAKKNFTETPLKEDKDNLE---HLVSPATSVHT 369  
 QY 514 GLASIIICDOLLEKEGSTKCM---RNIIQQLKNQVFLDDYKEIGSIPQVIGKILQK 569  
 Db 370 TVSDITGHQSVTDESEDNKCMSTPKTEIESKIEBISVSKSEISSVSVGK--EQ 427  
 QY 570 NNLSTRCLLIAYTNRRARDIRRYLEIKAFPPYNTVCLRLKLFSHNMTRLRKFMVYF 629  
 Db 428 NHTKQ---VAIETTPQOKVEKEDHL-----NLQGSFTEESTK----- 463  
 QY 630 GKNSQSLQKTPPLVVAICAMFQYPPDPSPDDVAV---FKSYMERLSLNKKAET 664  
 Db 464 ---QPISSNP-----STSSPDMTAAAGRVSSSPFDKILQCNFSP--- 502  
 QY 685 LKATVSSCGEIALKGFSCCFEFDNDDLAEGVDEDDLMCLMSKFTAOQLRPPTRLS 744  
 Db 503 -NSTIDFSNSISKRKNSE---EANDR-----NDENLMTPIPER-----K 538  
 QY 745 PAFQEFAGMLFLELDDSDREHODLGLYLKQINSPPMTVASVYNNFLVYVSSLSPTKAG 804  
 Db 539 RKFOEVLQSKNI--LVSTEDSHEPV---KVTEDSOTAIHVSKEFDLEN----- 582  
 QY 805 PKIYSHLLHYDNKESLENI--SENDYLRHPEISLQMLRGLMQICPOAVESVSEH 862  
 Db 583 ---KSMESQSIQLLSESEND---KPLDL----- 607  
 QY 863 LVLVALKTAYQSNVTAACSPFYVLOFLOGRTLTLGALNLQYFEDHDESLSLRSIHPIRG 922  
 Db 608 IPLAIKIR--KDLVSG---VLE--KCKSTSTSKTK--FD---TSYDPIE----- 646  
 QY 923 NKTSPRAHNSVLT-----ETCFDKSQVPTID-----ODYASAF-----EPNENERN 963  
 Db 647 ---KPRTEISEVLPPEKRAICDESGYTRVSDKRVSSPVSDKSENNWHEAN 703  
 QY 964 LAEKEDNVKSYMQRRA--DLSTG-YWKLSP-----KQYKIPCLEVDYNDIDVYGQD 1016  
 Db 704 SGHTVANNHSSLDPPPIYQPNELSGSYLKDLPDRNNGNSEKVTFOGDDINSKLOSKNN 763  
 QY 1017 LELIMTVFSASORI-ELHLNHSRGFTESIRPALFELSKASTYKSIKLELSAA--EQELL 1073  
 Db 764 QTVBAVNTETSDKLOEKAHNELENIKEKL-----TEVQVLSLSAFAFPQDEIK 814  
 QY 1074 LTPLSLELVSGTIOGSDQIFPMLDKFLKLELSVDLEGNINVFSEVIREEPNHNHEK 1133  
 Db 815 NSRISVQ---NGT-RSVSKNTPF-----KETKYDKIDNYSKKQV--ETSPGSCETSS 860  
 QY 1134 LLIDISAEYDPSKVLKIONS-----NLHYFHLKCNFFDFGSLMTMLVSC 1180  
 Db 861 AFAKTYAEKEVTSTI-----NLPSVRKPLDESYVDHSISFDFLCO--SSFLAPQTPYKSK 913  
 QY 1181 KKLTEIKSDFQAVPFAVSL-----PNTISLILMLEGOQFP-----D 1220  
 Db 914 HALPVEANAPWEPIDFSSLSLSPVPNPEVFNKLSEKELDMTEQWIKPMYAKCAKEFE 973  
 QY 1221 EETSEKFAVILGSLNLEELI 1241

Tue Oct 1 09:27:21 2002

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Page 9

Db 974 EACEKIEWLEEGKRAEEYI 994

Search completed: September 30, 2002, 15:05:37  
Job time: 228 sec

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[illegible]

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Db      2  KKKKGNOSMRSEAKRLKTEFTYDFPRSMTPQEMAAGFYHTGRLGVOCFCCSLTJFGN 61
QY      108 GLTRLPIEDHKRPHDCCGFLNKKDVGNIATKADIVKVLKSLRGKMRVQOEERLASFR 167
Db      62 SLKKLPIERHKKLRPECEFLQKDGKIDIRVKKRPEMLKMGARHEEARLESEFE 121
QY      168 MPEFYVQGISPCVLSAEAGFVTGKQDTPVOCFSCGCLGMWEGDDPMKEHAKMFKCEFL 227
Db      122 DMPEFAHGTSPRVLASAGFVTGKRDTPVOCFSCGCLGMWEGDDPMKEHAKMFKCEFL 181
QY      228 BEKSSSEETIYIOSYKGFVDITGEHFVMSWORELPMAVACNDISFAYBELRLDSFKD 287
Db      132 OSKSSSEETIYIOSYKGFVHTGEHFVMSWORELPMAVACNDISFAYBELRLDSFKD 287
QY      242 WPOESPVGVALVRAGFVTGKRDTPVOCFSCGCLGMWEGDDPMKEHAKMFKCEFL 301
Db      348 MKSSAEVTPDLOSRLCELETTSESNELEDSIAYGVYPERMAQGRQWFOAKMLNQL 407
QY      302 LKSSAEVTPDLOSRLCELETTSESNELEDSIAYGVYPERMAQGRQWFOAKMLNQL 407
Db      408 RAAYTSASRHMSLDISDLATDHLGCDLSIAKHSIKRQVEPRLVPEVFGNLNSVMC 467
QY      337 ----- 336
Db      468 VEGAGSGKTVLKKIAFLWASGCCPLRFQVLFYLSLSTRDEGLASICDQLLEKE 527
QY      337 ----- 336
Db      528 GSVTCKMKNIIQOLKNQVLFLLDDYKEICSIPOVIGLQKNHLSRTCLIAVTRNAR 587
QY      337 ----- 336
Db      588 DIRRYETLLETKAFPEFYNTVCLRLKLSHNMTRKRFVNGKNOLOKIQKRPVAA 647
QY      337 ----- 336
Db      648 ICAHMFQYRPFDPDVAVKFMYERLSLRKNAETAILKATVSSCGELALGFSCCFE 707
QY      341 ----- 340
Db      708 NDDDLAAGVDEDEDLTKLMSKFTAOALRPFYRFLSPARQEFLAGRLIELLSDROEH 767
QY      341 ----- 340
Db      768 QDLGLYHLKQINSPMTVASAYNNFLNYSLSRPTKAGPKIVSHLLVYNKESLENISEN 827
QY      341 ----- 340
Db      828 DDTLKHOREISLOMQLRGLWQICPAVFSWSEHLLVLAKTAYQSNVTAACSPVLOF 887
QY      341 ----- 340
Db      888 LOGRTLTGLALNLYFPDHPESLSLRSIHFPRLGNKTSPPRAHNSVLETCRKSQVPTID 947
QY      341 ----- 340
Db      948 QDYASAFEPNEMERMLAEKEDNVASYMDQMRASPOLSTGYMKLSPKQYKIPCLEVDYN 1007
QY      341 ----- 340
Db      1008 DIDVQODMELMTVFSASORIELHLSHGFEISIRPALSELKASYTKCSISKLELSA 1067
QY      341 ----- 340
Db      1068 ABOEILLTLPSLESLEVSGLTOSODOFPLDLKFLCLKELSDLEGNINVSVPREEFPN 1127
QY      341 ----- 340
Db      1128 FHHMEKLLIOISAEYDSKLVKLONSPRLHYEHLKCFPSDFGSLTMTLVSKKLETRK 1187
QY      341 ----- 340
Db      1187 VVKFIGNFRLNHFHLKCDPLSNCESESLMAVLAASCKKRLRETE 381

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## RESULT 2

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QY      1188 FDSFPAQVPAVSLPWFISLKLNLNLEGQFPDEETSEKFAVILIGSLSNUEELILTPGDG 1247
Db      382 FSGCSEFAMFVNILNPFVSLKLNLNLEGQFPDEETSEKFAVILIGSLSNUEELILTPGDG 441
QY      1248 IYVAKLIIOGCOQLNLNLSFFFTLNDSDVFEIATAVVAISGFORLLENLKSINRKTITE 1307
Db      442 IHOVAKLIIOGCOQLNLNLSFFFTLNDSDVFEIATAVVAISGFORLLENLKSINRKTITE 501
QY      1308 EGYRNFOLNLMWPMLOEILDSRHFTFCIKAAATVYKSLISOCVLRPLRLNMLSLD 1367
Db      502 EGYRNFOLNLMWPMLOEILDSRHFTFCIKAAATVYKSLISOCVLRPLRLNMLSLD 1367
QY      1368 ADDIALLNVMKERHPOSKYTLTILOKYLPPSPIT 1401
Db      562 EEDMKVINDYKERHPOSKYTLTILOKYLPPSPIT 595

```

Query Match 6.7% Score 486 DB 11 Length 589  
 Best Local Similarity 27.8% Pred. No. 3e-26; Mismatches 166; Indels 138; Gaps 23;  
 Matches 154; Conservative 75;

```

QY      41 EOKERAKMOKGYNSOMRSBAKRLKTFYVPEYSSWIP--QEMAAGFYFTVKGSGIQC 97
Db      12 KENKE--KMYDSCSCE-----LYRMSTYSAPFRGVYVSRSLARAGFYVGVNDKXVNC 62
QY      98 FCCSLILFGAGLRLPIEDHKRPHDCCGFLNKKDVGNIATKADIVKVLKSLRGKMRVQOEERLASFR 167
Db      63 FCCGLMLDMWKKQDSPTEKHNGFTYSCFVOTLLSGGLQSAKASTSPAKSRRAHSLPLEQ 122
QY      145 -----LCKSR-----LCKGKMY--OEEEARLASFRMMPYVQGISPCVLSAG 185
Db      123 GGIHSLSPNPLNSAAYDPSLRNPNCSYAMSTEARLSTSMMP--LSPLSPALAKAG 180
QY      186 FVETGKQDTPVOCFSCGCLGMWEGDDPMKEHAKMFKCEFLRKSSEETIYIOSYK 245

```

```
Db 191 FYYTGPGRVACFACGKLSNNEPNDPLSEHRRHPHCPELENTSEYQFS----- 232
Qy 246 FVDITGEHFNWSWVORELPMASAYCNDISIFAYEELRLDSFKDMPRESAVGAALAKAGLF 305
Db 233 -----VSNLSMQT-----HSARMSFTLYWPSSVLVQPOLASAGFY 268
Qy 306 YTGINDIVOCFCGCGGLEKMOEGDDPLDHTRCFPNCPFLQMKSSAEVTPDLQSR-GL 364
Db 269 YVDHNDVAKCFCCDGLRCWEPDDPWIEHAKWFPCEFLIMKGO-EVVDIQAARYPHL 327
Qy 365 CELLETTSESNEEDSIANGPIVPEMAOGAOMFOEAKNLNEOLRAAYTSASFRHMSLDI 424
Db 328 LEQLLSTSDTSEEN--ADPPVYHLGPGE-NM-EDAVMMNTPVYKA----- 369
Qy 425 SSDLATDHLGCDLSIASKHISKPYOEPLVLEPVEGNLSVNCV-----EGEAG 473
Db 370 ----ALD--MGFSRSLVRQTVOROI--LATGENTRTVSDIYALLNAEDEREEREKQ 420
Qy 474 SKRTVLKRIAFIPLWASGCCPLLRQVLYLSLSTRPEGLASITCDOLLEKESYTEM 533
Db 421 SEET-----ASGDSLIRKNRMALFOQLTCVIP-----ILDDL--EASVLT 461
Qy 534 CRRNIIOQLKNV 546
Db 462 EHDIIHQ-KTQI 473
```

## RESULT 3

```
Q90ZC6 3
ID Q90ZC6 PRELIMINARY: PRT: 589 AA.
AC Q90ZC6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT Cloning of cDNA for rat inhibitor of apoptosis protein 2.;
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA; 66777 MW; E6812FEE3EA31142 CRC64;
```

Query Match 6.7%; Score 486; DB 11; Length 589;  
Best Local Similarity 27.8%; Pred. No. 3e-26;  
Matches 154; Conservative 75; Mismatches 186; Indels 138; Gaps 23;

```
Qy 41 EEOKRRAKMOKGYSOMSEAKRLKTFVYEPYSSWIP---OEMAAGFTGVKSGIQC 97
Db 12 KKNKE--KKKYDFSCB-----LYRMSTYSAFPFGVPSESLRAGGYTYGVNDKVC 62
Qy 98 FCCSLILFGAGLTLRLPIEDHKRRHPDCGF--LNNKDVGNIAKYDIRVKN----- 144
```

```
Db 63 FCCGLIMDNMKGDSPTFKHRQFYPCSPFYQTLISGLQSAKKNSPAKSRFANSLPLEQ 122
Qy 145 -----LKS-----LRGKMR--QEEERKLASFNNPPYVIGISPCVLSENG 185
Db 123 GGIHSLPSNPINSLRAVEDFSLRMNPDSYAMSTEEARFLSYGMWP--LSFLSPAEILAKG 180
Qy 186 FVFTGKODTVOCFCGCGGLEKMOEGDDPWKEHAKWFPKCEFLRSKSSSEITQYIOSYKG 245
Db 181 FYYTGPGRVACFACGKLSNNEPNDPLSEHRRHPHCPELENTSEYQFS----- 232
Qy 246 FVDITGEHFNWSWVORELPMASAYCNDISIFAYEELRLDSFKDMPRESAVGAALAKAGLF 305
Db 233 -----VSNLSMQT-----HSARMSFTLYWPSSVLVQPOLASAGFY 268
Qy 306 YTGINDIVOCFCGCGGLEKMOEGDDPLDHTRCFPNCPFLQMKSSAEVTPDLQSR-GL 364
Db 269 YVDHNDVAKCFCCDGLRCWEPDDPWIEHAKWFPCEFLIMKGO-EVVDIQAARYPHL 327
Qy 365 CELLETTSESNEEDSIANGPIVPEMAOGAOMFOEAKNLNEOLRAAYTSASFRHMSLDI 424
Db 328 LEQLLSTSDTSEEN--ADPPVYHLGPGE-NM-EDAVMMNTPVYKA----- 369
Qy 425 SSDLATDHLGCDLSIASKHISKPYOEPLVLEPVEGNLSVNCV-----EGEAG 473
Db 370 ----ALD--MGFSRSLVRQTVOROI--LATGENTRTVSDIYALLNAEDEREEREKQ 420
Qy 474 SKRTVLKRIAFIPLWASGCCPLLRQVLYLSLSTRPEGLASITCDOLLEKESYTEM 533
Db 421 SEET-----ASGDSLIRKNRMALFOQLTCVIP-----ILDDL--EASVLT 461
Qy 534 CRRNIIOQLKNV 546
Db 462 EHDIIHQ-KTQI 473
```

## RESULT 4

```
Q9ESE9 4
ID Q9ESE9 PRELIMINARY: PRT: 602 AA.
AC Q9ESE9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes.;
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183430; AAG22970.1; -.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385E6A62DE5A CRC64;
```







InterPro: IPR001841; 2nf\_ring.  
 DR Pfam: PF00653; BIR: 3.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR: 3.  
 DR SMART: SM00184; RING: 3.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 KW Zinc-finger.  
 SO SEQUENCE 501 AA; 56578 MW; 4863699FE2E0C8CD CRC64;

Query Match 5.7%; Score 416.5; DB 11; Length 501;  
 Best Local Similarity 28.3%; Pred. No. 2.2e-21;  
 Matches 119; Conservative 60; Mismatches 162; Indels 79; Gaps 12;

60 EAKRLKFTVTEPYSSWIPQEMAAAGFYTGKSGIOGCCSLILFGAGLTRLPED--- 116  
 26 EFNRLKTFANPSSSPVASTLARAGFLYTGEGDTVOCFSCH-----AAVDRMQYDSAV 80  
 117 --HKRHPDCGFL-----LNKDVGNIAKYD 139  
 81 GRHRISPCAFINGFYFENGATOSTPGIONGYKSENCVGNRNHFDLDRSETHADYL 140  
 140 IR---VNLKSLRGKMRQEEARLASFRNMPFYVOGISCVLSEAGFVFTGQDTVO 196  
 141 LRTGOVVDISDTIYPRNPAMCSEARLKTQNPDYAH-LSPRELASAGLYTGTIDQVO 199  
 197 CFSCGGLGWMEEGDDPKWEHAKMFKCEFLSKSSSEITQYIOSYGFVDITGEHFN 256  
 200 CFCCGGLKMKWEPDRAMSEHRHFPNCFVLRN-----VAVRESGV 244  
 257 SWQRELPMASAYCNDSTIFAYEELRLDSFKDMPRESAVGVALAKAGLFTYGIQDIYOCF 316  
 245 S--DRNFPNSTNSPRNPAAVEYDARIYFTGM--LYSNKQDLNAGFYALGEGDKYKCF 300  
 317 SCGGCLEKNOEGDDPLDHTRCFPCNPCLQNNKSSAEVTPDLQSRGELCELLETTS--- 373  
 301 HCGGGLTDMKPSDEPWEHAKMFKCEFLSKSSSEITQYIOSYGFVDITGEHFN 359  
 374 ---SNLEDSIAVGPIVPEMAOGEAOMFOEAKNLNOLRAATVSFRHMSLIDISDLAT 430  
 360 SVTKRIDTIFQNPVQVQALRMGFNFNDIKTMEKLD---TSGS-NYLSLEVLADIADLV 415

RESULT 9  
 Q9ESF0 PRELIMINARY; PRT; 496 AA.  
 AC Q9ESF0:  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 OS INHIBITOR OF APOPTOSIS PROTEIN 3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.,  
 RT Cloning and Characterization of the Rat Homologs of the Inhibitor of  
 RT Apoptosis Protein 1, 2, and 3 Genes.  
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AF183429; AAG22969.1;  
 DR HSSP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR: 3.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR: 3.  
 DR SMART: SM00184; RING: 3.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.

KW Zinc-finger.  
 SO SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 5.6%; Score 409.5; DB 11; Length 496;  
 Best Local Similarity 28.1%; Pred. No. 7e-21;  
 Matches 118; Conservative 60; Mismatches 163; Indels 79; Gaps 12;

60 EAKRLKFTVTEPYSSWIPQEMAAAGFYTGKSGIOGCCSLILFGAGLTRLPED--- 116  
 26 EFNRLKTFANPSSSPVASTLARAGFLYTGEGDTVOCFSCH-----AAVDRMQYDSAV 80  
 117 --HKRHPDCGFL-----LNKDVGNIAKYD 139  
 81 GRHRISPCAFINGFYFENGATOSTPGIONGYKSENCVGNRNHFDLDRSETHADYL 140  
 140 IR---VNLKSLRGKMRQEEARLASFRNMPFYVOGISCVLSEAGFVFTGQDTVO 196  
 141 LRTGOVVDISDTIYPRNPAMCSEARLKTQNPDYAH-LSPRELASAGLYTGTIDQVO 199  
 197 CFSCGGLGWMEEGDDPKWEHAKMFKCEFLSKSSSEITQYIOSYGFVDITGEHFN 256  
 200 CFCCGGLKMKWEPDRAMSEHRHFPNCFVLRN-----VAVRESGV 244  
 257 SWQRELPMASAYCNDSTIFAYEELRLDSFKDMPRESAVGVALAKAGLFTYGIQDIYOCF 316  
 245 S--DRNFPNSTNSPRNPAAVEYDARIYFTGM--LYSNKQDLNAGFYALGEGDKYKCF 300  
 317 SCGGCLEKNOEGDDPLDHTRCFPCNPCLQNNKSSAEVTPDLQSRGELCELLETTS--- 373  
 301 HCGGGLTDMKPSDEPWEHAKMFKCEFLSKSSSEITQYIOSYGFVDITGEHFN 359  
 374 ---SNLEDSIAVGPIVPEMAOGEAOMFOEAKNLNOLRAATVSFRHMSLIDISDLAT 430  
 360 SVTKRIDTIFQNPVQVQALRMGFNFNDIKTMEKLD---TSGS-NYLSLEVLADIADLV 415

RESULT 10  
 Q9DDN2 PRELIMINARY; PRT; 324 AA.  
 AC Q9DDN2:  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 OS APOPTOSIS INHIBITOR CH-1AP1 (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.,  
 RT "The apoptosis inhibitor ch-1ap1 is a direct transcriptional target of  
 RT v-Ret and c-Rel."  
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF111289; AAG42316.1;  
 DR HSSP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR: 3.  
 DR SMART: SM00238; BIR: 3.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
 FT NON\_TER  
 SO SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;

Query Match 5.3%; Score 386; DB 13; Length 324;  
 Best Local Similarity 28.6%; Pred. No. 1.8e-19;  
 Matches 95; Conservative 41; Mismatches 108; Indels 88; Gaps 7;

60 EAKRLKFTVTEPYSSWIPQEMAAAGFYTGKSGIOGCCSLILFGAGLTRLPEDHKR 119  
 117 --HKRHPDCGFL-----LNKDVGNIAKYD 139

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Db 30 ELYRMSTSTFPVNVSEBRLARAGFYTGVDVKCFSCGLVLDNMQPDNAMEKHQ 89
QY 120 FHPDGFLLN-----KDYGN----- 135
Db 90 YPSCSFVQNMILSNLGLSTHSAPLVASNLSPSLSMTLSPSEFOGYGFSGFSRSP 149
QY 136 -----AKYDIRVKNLRLRGKMRQOEERARLSPFVYOGISPCVLSEAGFVF 188
Db 150 QDPVTRAEEDL--SHLSKSLNPSM--STEARLRTFHAMP--LMPFSLPTLAKAGLY 203
QY 189 TKGQDVOCFSCGCLGNWEGDDPMKEHAKWPKCEFLRSKSSSEITQYI0SYKGFVD 248
Db 204 LGTAKVACFTCGGOLSNWEPKDNAMSEHRHFPNCPFEVN----- 244
QY 249 ITHGFVMSWQRELPMASAYCNSIFAVEELRLDSFKDMPRESAVGVALAKAGLFTG 308
Db 245 -----LMKRDQ--SFVNSVNTMOTHEARVFTFMPTFRIPVQPEQLADAGFYVG 292
QY 309 IKDIQVCFSCGCLGKMOEGDDPLDHTRCFP 340
Db 293 RMDVYKCFCCGCLRGWESGDDPMIEHAKWFP 324

RESULT 11
Q960U3 PRELIMINARY: PRT: 498 AA.
ID 0960U3
AC 0960U3
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE LD34777P.
GN IAP2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayanl A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RA Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: AY01844; AAK93268.1;
DR EMBL: AY01844; AAK93268.1;
SQ SEQUENCE 498 AA: 54537 MW: 0D0303DB2B26FA22 CRC64;

Query Match 4.6%; Score 336; DB 5; Length 498;
Best Local Similarity 27.8%; Pred. No. 1.3e-15;
Matches 98; Conservative 54; Mismatches 125; Indels 76; Gaps 13;

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QY 332 LDDHTRCFPCNPFLONMKSAFVTPDLOSREGICELLTTSNSLDESIANCP 384
Db 266 WEHAKWSKCFQVILLARGPAYVS-----EVLATTA-ANASSOPATAP 307

RESULT 12
Q09123 PRELIMINARY: PRT: 87 AA.
ID 009123
AC 009123
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1C (NEUONML APOPTOSIS
DE INHIBITOR PROTEIN, RELATED SEQUENCE 5) (FRAGMENT).
DE BIRIC OR NAIP3 OR NAIP-RS3.
CN BIRIC OR NAIP3 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the Lgl1 critical interval and contains multiple copies of Naip
RT exon 5."
RL Genomics 38:405-417(1996).
CC -! SIMILARITY: CONTAINS 1 BIR DOMAIN (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
DR EMBL: U66328; AAC52976.1; -.
DR HSSP: Q13490; 10BH.
DR MGP: MGI:1298225; Birc1c.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 1.
DR SMART: SM00238; BIR; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; PARTIAL.
DR PROSITE: PS01443; BIR_REPEAT_2; 1.
FT NON_TER 1
FT NON_TER 87
SQ SEQUENCE 87 AA: 9997 MW: B184943B3BC52E3A CRC64;

Query Match 4.4%; Score 325; DB 11; Length 87;
Best Local Similarity 70.1%; Pred. No. 5.7e-16;
Matches 61; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

```

RC STRAIN-BRED LECHORN; TISSUE=SPLEEN;  
 RX MEDLINE-21158006; PubMed-11261557;  
 RA Zhou H., Liu W., Lamont S.J.;  
 RT "Genetic variation among chicken lines and mammalian species in  
 specific genes";  
 RL Poul. Sci. 80:284-288(2001).  
 DR EMBL: AF221082; AAF5319.1; -.  
 DR HSSP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 2.  
 DR SMART: SM00238; BIR; 2.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 2.  
 FT NON\_TER 1 1  
 FT 195 195  
 SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 4.4%; Score 323.5; DB 13; Length 195;  
 Best Local Similarity 35.1%; Pred. No. 2.4e-15;  
 Matches 72; Conservative 29; Mismatches 63; Indels 41; Gaps 7;

OY 46 RAKQKGYNSQMRSEARLKTFTYEPYSSWIRQEMAAAGFTYGVKSGIQCCSLLIF 105  
 DB 19 RSKL---HNPSSMTEEARLRTFTNAM-PLMFLSPTELAKAGLYLGTADKYACFTC----- 69  
 OY 106 GAGLTRLPDIED-----HKRPHDPCGFLLNK-----DVCNIAKYDIRVKNLKSRLRGK 153  
 DB 70 GGQLSNWEPKDNAMSEHRRHFPNCPEVENLMRDQPSFNNSNT----- 112  
 OY 154 MRQEEARLASFRNMPFYQGISPCVLSFAGVFTGKQDTVOFCSCGCLGMWEGDDP 213  
 DB 113 --MOTHEARVKTFTNMPTRIP-VQPEQLADAGFYVGRNDVVCFCDDGGLRCMESGDDP 169  
 OY 214 WKEHAKWPCPCFLRSKKSSEITQ 238  
 DB 170 WIEHAKWPCPCFLRSKKSSEITQ 194

RESULT 14  
 OY1A69  
 ID 091A69 PRELIMINARY; PRT; 197 AA.  
 AC 091A69;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2001 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRED FAYOUMI; TISSUE=SPLEEN;  
 RX MEDLINE-21158006; PubMed-11261557;  
 RA Zhou H., Liu W., Lamont S.J.;  
 RT "Genetic variation among chicken lines and mammalian species in  
 specific genes";  
 RL Poul. Sci. 80:284-288(2001).  
 DR EMBL: AF221083; AAF5320.1; -.  
 DR HSSP: Q13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 2.  
 DR SMART: SM00238; BIR; 2.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 2.  
 FT NON\_TER 1 1  
 FT 197 197  
 SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 4.4%; Score 323.5; DB 13; Length 197;

Best Local Similarity 35.1%; Pred. No. 2.5e-15;  
 Matches 72; Conservative 29; Mismatches 63; Indels 41; Gaps 7;  
 OY 46 RAKQKGYNSQMRSEARLKTFTYEPYSSWIRQEMAAAGFTYGVKSGIQCCSLLIF 105  
 DB 20 RSKL---HNPSSMTEEARLRTFTNAM-PLMFLSPTELAKAGLYLGTADKYACFTC----- 70  
 OY 106 GAGLTRLPDIED-----HKRPHDPCGFLLNK-----DVCNIAKYDIRVKNLKSRLRGK 153  
 DB 71 GGQLSNWEPKDNAMSEHRRHFPNCPEVENLMRDQPSFNNSNT----- 113  
 OY 154 MRQEEARLASFRNMPFYQGISPCVLSFAGVFTGKQDTVOFCSCGCLGMWEGDDP 213  
 DB 114 --MOTHEARVKTFTNMPTRIP-VQPEQLADAGFYVGRNDVVCFCDDGGLRCMESGDDP 170  
 OY 214 WKEHAKWPCPCFLRSKKSSEITQ 238  
 DB 171 WIEHAKWPCPCFLRSKKSSEITQ 195

RESULT 15  
 OY09119  
 ID 009119 PRELIMINARY; PRT; 87 AA.  
 AC 009119;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE NEURONAL APOPTOSIS INHIBITORY PROTEIN RELATED SEQUENCE 1  
 DE (FRAGMENT).  
 GN BIRC1-RS1 OR NAIP-RS1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129/SVJ;  
 RX MEDLINE-97131520; PubMed-8975718;  
 RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,  
 RA Kunkel L.M., Dietrich W.F.;  
 RT "The mouse region syntenic for human spinal muscular atrophy lies  
 within the 1qnl critical interval and contains multiple copies of Naip  
 exon 5.";  
 RL Genomics 38:405-417(1996).  
 DR EMBL: U66324; AAC52972.1; -.  
 DR HSSP: Q13490; 10BH.  
 DR MGP: MGI:109439; Birc1-rs1.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 1.  
 DR SMART: SM00238; BIR; 1.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 1.  
 FT NON\_TER 1 1  
 FT 87 87  
 SQ SEQUENCE 87 AA; 9958 MW; E601604230BCID25 CRC64;

Query Match 4.4%; Score 320; DB 11; Length 87;  
 Best Local Similarity 69.0%; Pred. No. 1.3e-15;  
 Matches 60; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 82 AAAGFTYGVKSGIQCCSLLIFGAGLTRLPDIEDHKRPHDPCGFLLNKDGNIAKYDIR 141  
 DB 1 AAAGFTYGVKSGIQCCSLLIFSTRLRKLPDENHKKLRCECFDQGVGNIGKXYDIR 60  
 OY 142 VKNLKSRLRGKMRQEEARLASFRN 168  
 DB 61 VKSPEKMLRGKARTHEEARLESFED 87

Search completed: September 30, 2002, 15:06:30  
 Job time: 186 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 30, 2002, 14:59:19 ; Search time 41.9 Seconds  
(without alignments)  
3719.249 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 7308

Sequence: 1 MAQQKASDERISQFDHNL.....SKYLLIKKWLFPSPILQK 1403

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*  
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19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*  
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*  
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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	7308	100.0	1403	18 AAM20032
2	7308	100.0	1403	20 AAT14075
3	7308	100.0	1403	20 AAT09539
4	7308	100.0	1403	21 AAT88053
5	7284	99.7	1403	18 AAM20033
6	6691	91.6	1295	20 AAT14080
7	6691	91.6	1295	20 AAT09540
8	6373.5	87.2	1232	17 AAT88217
9	661	9.0	1204	22 AAT02881
10	654	8.9	1070	22 AAT67527
11	653	8.9	1024	22 AAT02880

12	566	7.7	841	22	AAM23595
13	545.5	7.5	118	21	AAB53493
14	536.5	7.3	738	22	AAG67526
15	462	6.3	618	18	AAM19746
16	462	6.3	618	18	AAM19583
17	462	6.3	618	18	AAW13545
18	462	6.3	618	19	AAW69296
19	462	6.3	618	20	AAV33998
20	457.5	6.3	612	18	AAW13555
21	457.5	6.3	612	18	AAW69299
22	441.5	6.0	591	18	AAW19586
23	440	6.0	600	19	AAW69298
24	437.5	6.0	496	18	AAW19584
25	437.5	6.0	496	19	AAW69297
26	436.5	6.0	604	18	AAW19747
27	436.5	6.0	604	18	AAW13546
28	436.5	6.0	604	20	AAV32703
29	436.5	6.0	604	20	AAV33997
30	435	6.0	1141	22	AAW69694
31	431.5	5.9	496	18	AAW19745
32	431.5	5.9	604	18	AAW19582
33	431.5	5.9	604	19	AAW69295
34	427.5	5.8	602	18	AAW19585
35	407	5.6	497	21	AAV59451
36	403	5.5	497	18	AAW19581
37	403	5.5	497	19	AAW69294
38	403	5.5	497	21	AAV59985
39	354	4.8	642	22	AAW25640
40	340.5	4.7	438	17	AAW04583
41	336	4.6	498	22	AAW62863
42	335	4.6	498	18	AAW19748
43	320	4.4	60	21	AAW01849
44	318.5	4.4	306	22	AAU02925
45	304.5	4.2	438	22	AAW48191

## ALIGNMENTS

RESULT 1					
AAM20032 standard; Protein: 1403 AA.					
ID	AAW20032				
AC	AAW20032				
XX	06-OCT-1997 (first entry)				
XX					
DE	Neuronal apoptosis inhibitor protein (NAIP).				
XX					
KW	Neuronal apoptosis inhibitor protein; NAIP; diagnosis: therapy; cancer; AIDS; amyotrophic lateral sclerosis; spinal muscular atrophy.				
XX					
OS	Homo sapiens.				
XX					
PN	W09726331-A2.				
XX					
PD	24-JUL-1997.				
XX					
PF	17-JAN-1997; 97WO-1B00142.				
XX					
PR	19-JAN-1996; 96GB-0001108.				
XX					
PA	(UYOT-) UNIV OTTAWA.				
XX					
PI	Korneluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K; WPI: 1997-385335/35.				
XX					
DR	N-PSDB: AAT71265.				
XX					
PT	New neuronal inhibitor of apoptosis - useful for diagnosing and treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis				
XX					

Murine EGF encoded  
Human colon cancer  
Amino acid sequenc  
Human inhibitor of  
Human apoptosis in  
Human c-IAP1. Hom  
Human HIAP-2 prote  
Human cellular inh  
Murine c-IAP. Mus  
Murine HIAP-2 prot  
Mouse apoptosis in  
Murine HIAP-1 prot  
Mouse apoptosis in  
Murine XIAP protei  
Human inhibitor of  
Human c-IAP2. Hom  
Human cellular inh  
Human AP12-MLT chl  
Mouse inhibitor of  
Human apoptosis in  
Human HIAP-1 prote  
Mouse apoptosis in  
Human XIAP protein  
Human apoptosis in  
Human XIAP protein  
Human X-linked inh  
Human protein sequ  
Human inhibitor of  
Drosophila melanog  
Drosophila inhibit  
Human secreted pro  
Angiotensin conver  
Drosophila mutant

PS Claim 41; Fig 6A-I; 102pp; English.  
 XX  
 CC Novel human neuronal apoptosis inhibitor protein (AAM20032), or NAIP,  
 CC is a negative regulator of apoptosis, partic. neuronal apoptosis  
 CC and, when deficient or absent, contributes to neurodegenerative  
 CC phenotypes such as spinal muscular atrophy (SMA) and amyotrophic  
 CC lateral sclerosis. Its amino acid sequence was deduced from a  
 CC cDNA clone (AA71265) obtd. from a human foetal spinal cord cDNA  
 CC library. NAIP polypeptides, esp. those containing at least two  
 CC BIR (baculovirus iAP repeat) domains, can be expressed in host  
 CC vector systems and used to increase or induce apoptosis in host  
 CC treatment of AIDS, neurodegenerative disease, myelodysplastic  
 CC syndromes or ischaemic injury, to screen for (anti)agonists, or to  
 CC produce antibodies useful for inhibiting apoptosis.  
 SO Sequence 1403 AA;

Query Match 100.0%; Score 7308; DB 18; Length 1403;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATQKASDERISQFDHNLPELSALLGLDAVOLAKELSEEROKRAKQKYNQMSHSE 60  
 DB 1 matqkasderisqfdhnlpeelsallgldevqlakelseeqkerakmqgynsqmrse 60  
 QY AKRLKFTVYEPYSSWIPQEMAAAGFYTGVSAGIQCSCSLIFGAGLITRLPTEDHKRF 120  
 DB 61 akrlkftvyepyswipemaaagfytgvsagiqcfcscslifgaglitrlptedhkrf 120  
 QY 121 HPDCCGLLKKDVGNTAKKDIRKVNLSRLGGMKRYQEEEARLASFRRMPPYVGISPCV 180  
 DB 121 hpdcgllkkdvgntakkdirvknlsrlggmkryqeeearlasfrmpfyvgispcv 180  
 QY 181 LSEAGFVFTGKODTVQCSGCGCLNMWEGDPPKKEHAKKPPKCEFLSKSSSEITQYI 240  
 DB 181 lseagfvftgkodtvqcsgccgclnmwegdppkkehakkppkceflskssseitqyi 240  
 QY 241 OSYKGFVDTGHEFVNSVQRELPMAAAYCNDISIFAVEELRLDSFKMPPRESAVGVALA 300  
 DB 241 osykgfvdthgefhnsvqrelepmasaycndisifaveelrldsfkmpresavgvala 300  
 QY 301 KAGLFTYTGKIDIVQCFSGCGCLEKMGCDPDLDDHTRCFNCPFLQNMKSSAEVTPDLQS 360  
 DB 301 kaglfytygkidiyvcfsgcgclekmgcdpdlddhtrcfncpflqnmkssaevtpdlqs 360  
 QY 361 RGEICELLETTSESNLEDSIAVGPVPEMAQGEAOMFOEAKNLEOLRAAYTSASFRHMS 420  
 DB 361 rgeicellettseesnledsiavgpvpemaqgeaomfoeaknleolraaytsasfrhms 420  
 QY 421 LLDISSDLATDHLGCDLSIAASKHISKPVQEPVLVLPVFGNTLNVACVCEAGSGKTVLL 480  
 DB 421 lldissdlatdhlgcdlsiaskhiskpvqepvlvlpvfgntlnvavcveagsgktvll 480  
 QY 481 KKAFLMASGCCPLNRFOLVFLYLSSTRPDEGLASTICDOLKEGSVTMCRAKNTIQ 540  
 DB 481 kkaflmasgccplnrfolvflylsstrpdeglasticdolkegsvtmcraknitiq 540  
 QY 541 QLNQVLFLLDDVKEICSPVYIGKILQKNHLSRCTLIAVTRNARDIRYLETILEIK 600  
 DB 541 qlnqvlfllddvkeicspvyigkilqknhlsrctliaavtrnardiryletileik 600  
 QY 601 APFFYTVTCILRLKFSNNTRLRKKEFVYGGKQSLQKOTKPTLPVAAICAMFQPEDPS 660  
 DB 601 apffytvtcillrlkfsnntrlrkkefvyyggkqslqkotpptlpvaaicamfqpeds 660  
 QY 661 PDDVAVFYSYMERLSLRKKAFAEILKATVSSGCELALKGFFSCFENNDDDLAAGVDED 720  
 DB 661 pddvavfysymerlslrkkafaeilkatvssgcelalkgffscfennddllaagvded 720  
 QY 721 EDLTCNLSKFTQAQLRPFYRFLSPAPQEFLAGRLTELLDSDQEQMODLGLYHLKQINS 780  
 DB 721 edltnclnskftaqqlrpfyrfllspapqeflagrltelldsdqeqmodlgllyhlkqins 780

QY 781 PMWTSAYNNFLNVYSSLPSTKAGPKIVSHLHLVDNKSESLENTSEDDLYLKHPETSLQ 840  
 DB 781 pmwtsaynnflnvyslpstkakgpkivshlhlvdnkseleentseddylykhpetslq 840  
 QY 841 MQLLGLNQICPOAVFVSWSHLLVNLKTRVGSNTVAAACSPVLOFLQGRITLGLALNL 900  
 DB 841 mqlglglngicpovfvswwshllvnlktrvgstnvaaacspvloflqgritlglaln 900  
 QY 901 QYFDPHSESLILRSIRHPTRGNKTSPPRAHVSYLETFQDSQVPTDQOYASAFEMKEM 960  
 DB 901 qyfdphseslilrsirhptrgnktspprahvsyletfqdsqvptdqoyasafemkem 960  
 QY 961 ERNLAEEKDANKSYMDQGRASPDLSGTWKLSPKOYKIPCELVNDVIDVYGOMLETI 1020  
 DB 961 ernlaeekdnksymdqgraspdlsqtwklspsykkipcelevndvidvygomleti 1020  
 QY 1021 MTFVSASQRIELHLNLSRGFIESIRPALSELKASVTKCSIKSLLSAABQELLTLPSLE 1080  
 DB 1021 mtfvsasqriehlhlnsrgfiesirpalselekasvtkcsikslsaaqelltlpsle 1080  
 QY 1081 SLEVSQTIOSODQIFPNLDKFLCLAKELSVDEGNTNVESVIPLEEPNPFHMEKTLIOISA 1140  
 DB 1081 slevsqtiqsdqifpnldkflclakelsvdegntnvsvipleepnpfhmehtlioisa 1140  
 QY 1141 EYDPSKLVKLIONSPLHVFHLKCNFFSDFGSLMTMLVSCKLTETIKRSDSFPQAVPVA 1200  
 DB 1141 eydpsklvklionsplhvfhlkcnffsdfgslmtmlvsccktetirksdsfpqavpva 1200  
 QY 1201 SLPNFISLITLNEGOQPDDETSERKFAVYIGSLSNLEELLPTGQGIYRVAKLIIQCCQ 1260  
 DB 1201 slpnfislitlnegoqpddeyserkfavyigslsnleellptgqgiyrvakliiqccq 1260  
 QY 1261 QHCLRLVSFFFTLNDSDVETIAKVAISGFOKLENTKLSTINHITTEGVRNFEQALDNM 1320  
 DB 1261 qhclrlvsffftlndsdvetiakvaisgfoklenklstinhittegvrnfeqaldnm 1320  
 QY 1321 PNLQELDISRHPTECIRKQATTVKSLSCVRLRLRLRNKLWSLWDADITALNWKER 1380  
 DB 1321 pnlqeldisrhptecirkqatvkslscvrlrlrlrnklwslwdaditalnwkerr 1380  
 QY 1381 HPQSKYTLTILQKWILPSPPIQK 1403  
 DB 1381 hpqskytltllqkwilpsppiqk 1403

## RESULT 2

AAV14079 standard; Protein; 1403 AA.

AC AAV14079:

DT 20-JUL-1999 (first entry)

DE Gonadotropic hormone protein sequence.

KW Gonadotropic hormone; excessive ovulation animal; transgenic animal;

KW totipotent cell; somatic cell chromosome.

OS Homo sapiens.

PN JP11113444-A.

PD 27-APR-1999.

PF 14-OCT-1997; 97JP-0280830.

PR 14-OCT-1997; 97JP-0280830.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX (SAKA-) SAKAI H.

DR WPI; 1999-320709/27.

DR N-PSDB: AAX58000.  
XX An excessive ovulation animal - useful for improving the  
PT productivity of animals  
XX  
PS Claim 3: Page 11-14; 18pp; Japanese.  
XX  
CC This sequence represents a gonadotropic hormone.  
CC The invention relates to an excessive ovulation animal, which is a  
CC transgenic animal with a totipotent cell containing a DNA fragment  
CC containing a promoter sequence and a gonadotropic hormone coding  
CC sequence. The DNA fragment is in the somatic cell chromosome. The  
CC excessive ovulation animal is useful for improving the productivity of  
CC animals. The method can improve the productivity of a useful animal.  
XX  
SO Sequence 1403 AA;  
  
Query Match 100.0%; Score 7308; DB 20; Length 1403;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MATQKASDERISQPDHMLPELSALGLDAVQAKLELEEDOKERAKKQKQNSQMRSE 60  
DB 1 matqkaaderisqfdhmlpeltsallglavqakelleeeqkerakmqkqnsqmrse 60  
QY 61 AKRLKFTPTYPEPSWIRQEMAAAGFTFGVKSIGQCCSLILGAGCITRLPIEDHKRF 120  
DB 61 akrllkftptypepswirqemaaagftfgvksiqccscslilgagcitrllpiedhkrf 120  
QY 121 HPDGFELINKDVGNIATKDYIRVKNLKSRLRGKMRYOEEEARLASRMPFVVOGISPCV 180  
DB 121 hpdgfeilinkdvgniatkdyirvknlsrlrgkmryoeeearlasrmpfvvoGISPCV 180  
QY 181 LSEAGFVFTGKODFVQCFSCGCGCLGNWEEGDPMKEHAKWPKCFELRSKSSSEETIQT 240  
DB 181 lseagfvftgkodyvqcfscgcgclgnweegdpmkewpkcfelrskssseetiqt 240  
QY 241 OSYKFFVDTGHRFNYSWQRELPMASAYCNSITAFYELRLDSRKDWREAVGVAALA 300  
DB 241 osykffvdtghrfnyswqrelpmasaycnsitafyelrldsrkdwrereavgvaala 300  
QY 301 KAGLFYTGKIDIVQCFSCGCGCLEKMOEGDDPLDHTRCFPNCPFLQNMKSSAEVTPDLOS 360  
DB 301 kaglfytgkidyvqcfscgcgclekmoegddpldhtrcfpncpflqnmkssaevtPDLOS 360  
QY 361 RGEIACELETTSESNEEDSIAVGPIVPEMAQGEAQMFOEAKNLNDOLRAAYTSASFRRHS 420  
DB 361 rgeiaceleTTSESNEEDSIAVGPIVPEMAQGEAqwfgeaknlneqlraaytsasfRRHS 420  
QY 421 LLDISSDLATDHLGCDLSIAKSHISKPYQEBLVLPVFGNLSNVCVGEAGSGKTIVLL 480  
DB 421 lldissdlatdhlhgcdlsiasKshiskpyqebLvpvfgnlsnvcvgeagsgktivll 480  
QY 481 KKAIAFLMASGCCPLNRFOLVYLSLSSTRPDEGLASIIDCDLLEKESVTMCMMKNITQ 540  
DB 481 kkaiaflmasgccplnrfolvylsLSSTRpdeglasiicdLlekesvtemcmnitq 540  
QY 541 QLKNOVELLDYKEICSTIPQYIGKLIQKNHLSRTCLLIAVBTNRADIRRYLETLEIK 600  
DB 541 qlknovelldykeicstipQyigkLIQKNHLSrtclliavbTNRADIRRYletleik 600  
QY 601 AFFEYNTWCILBKLSHNNTRLRKFMVYFGKNOSLOKTKTFLFAALCAHMFQVPRDS 660  
DB 601 affeyntwcilBKLSHNNTRLRKFMVYfgknosLOKTKTflfaALCAHmfqVPRDS 660  
QY 661 FDDVAVFKSYMERLSLRNKATAEILKATVSOCGELALKGFSCCFEFNDDDLAEGVDED 720  
DB 661 fddvavfksymerLSlrnkataEilkaTVSOCgeLaLKgfscCFEFndddlaegvded 720  
QY 721 EDLTYCMLSKFTAQRLRPYRFLSPAFOEFLAGMRLIELLSDROEHODLGLYHLKQINS 780  
DB 721 edltycmlskftaqRLrpyRFLSPAFOEflAGMRLIELlSDROEHODlglYhlkQINS 780

QY 781 PMMTVASAVNNFLNYSVSLPSTKAGPKIVSHLHLVDNKNESLENISENDYLKHQPEISIQ 840  
DB 781 pmmTVASAVnnflNySVslpStkaGPKivshLhlvdnKNesLeniseNdylKhqPeisIQ 840  
QY 841 MOLLGLMIOICPOAFESWVSEHLVLALTKTAYQSMVVAACSPFVQFLOGRTLTGALML 900  
DB 841 mllGLMIOICPOafesWVsehlVLAltkTayqSMVVAACSPfVQfLOGrtLTgAlML 900  
QY 901 QYFDPHESLSLSRSIHPRIRGNKTSPPRAHFSVLETCFDSQVPTIDODYASAFPMNEM 960  
DB 901 qyfdphesLSLSrsIHprIRGNkTSppRAHfSVleTCfDSqVptIDODyASAFpmNEM 960  
QY 961 EBNLAEKEDNVKSYMMDQKRRASPDLSGTGKWSLSPQYKIPCELVYVNDIDVYGOMLETL 1020  
DB 961 ebnlaEKEDNVkSYMMDQKRRASPDLSgtGkWSlSPQyKIPceLVyVNDIDVygOMLETL 1020  
QY 1021 MTFVSAORIEHLNHSRGFIESIRPALELSKASVTKCSISKLELSAAEQELLTLPSLE 1080  
DB 1021 mtfvsaORIEhlNHSrgfIESIRpALElSKASvTKCSiSkLELSAAEQellTLpSLE 1080  
QY 1081 SLEVSQGTIQSODQIFPNLDKFLCLKELSVDELGNINVSVPIDEEPNNHMEKLLIQISA 1140  
DB 1081 slevsqgtIQsODQIFpNLdKfLCLKELsvDELgNINvsVPIDEEPnnHMEKLLIQISA 1140  
QY 1141 EYDPSKIVKLIONSPNLAHVFKCNPFSDSGSLMTMLVSCKLTETIKFSDFSFOAVPFA 1200  
DB 1141 eydpskivKLIONSPnlAHvFKCNpfSDsgSLMTmlVSCkLTETIKfsDFSfoAVPFA 1200  
QY 1201 SLPNFSLKILMLGEOQFPDEETSEKFAVTLGSLSNLEELIPTDGIYRVAKLLIIOCO 1260  
DB 1201 slpnfSLKilMLGEOqFPDEETseKFAVtlGslSNleELIPTdGIYrvAKllIIOCO 1260  
QY 1261 QULHCLRVLSFFRTLNDOSVVEIAKVAISGFOKLENKLSINHKTTEBQYRNFPQALDMM 1320  
DB 1261 qulhclrvLSffRTlNDOSvVEIAKVAISGfoKLENkLSINHktTEBqYRNfPQALDMM 1320  
QY 1321 PNLGELDISRHFTFECIKKAAOTVKSLSOCVLRPLRILNMLSWLLDADIDLNVNKR 1380  
DB 1321 pnlGELdisRhFTfECIKKAAOTvKSLSocVLRpLRILnMLSWllDADIDLNVnKR 1380  
QY 1381 HPQSKYLTLLQKMLLPFSPIQK 1403  
DB 1381 hpqskYLTllQkMLLPfsPIqK 1403  
  
RESULT 3  
AAY09539  
ID AAY09539 standard; Protein: 1403 AA.  
XX  
AC AAY09539;  
XX  
DT 20-JUL-1999 (first entry)  
XX  
DE Human apoptosis inhibiting protein #1.  
XX  
KW Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;  
KW spinal muscular atrophy.  
XX  
OS Homo sapiens.  
XX  
PN JP11116599-A.  
XX  
PD 27-APR-1999.  
XX  
PF 14-OCT-1997; 97JP-0280831.  
XX  
PR 14-OCT-1997; 97JP-0280831.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
WI PI: 1999-323531/27.  
DR N-PSDB: AAX56272.

XX New Apoptosis Inhibitory protein - useful for determining mechanism  
 PT of various apoptotic diseases e.g. human spinal muscular atrophy  
 XX  
 PS Claim 1; Page 4-8; 16pp; Japanese.

XX The present sequence represents a human apoptosis inhibitory protein.  
 CC The apoptosis inhibitory protein is useful for the elucidation of  
 CC the mechanism of various apoptotic diseases such as human spinal  
 CC muscular atrophy and the diagnosis, the prevention and the treatment  
 CC of such diseases.  
 XX  
 SQ Sequence 1403 AA:

Query Match 100.0%; Score 7308; DB 20; Length 1403;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MATQKASDERISQEDHNLPELSALGLDAVQALAKLEEEERAKMKQKGYNSQRSE 60  
 1 mtqgkaaderisqedhnlpeelsalgladvqlakelleeeeqkerakmqkgynsqmrse 60  
 61 AKRLTFYVYEPYSSWIMQEMAAAGFTYGVKSGICQFCSSLIFGAGLRLEIEDHKRF 120  
 61 akrltfvtcyepyswipqemaagfitygvksqigcfcssliffagltrlriedhkrf 120  
 121 HPDCGFLLNKDVGNIAKDIKVKNLKSRLLGSKRWKQEEARLASFRNMPFYVQGISPCV 180  
 121 hpdcgfllnkdvgniakdikvknlsrllgskrkwqeeearlasfrnmpfyvgispcv 180  
 181 LSEAGFVETGKODTVQCFSCGCCGCKMWEEDDPMKEMHAKMPCCEFLRKSKSEETQYI 240  
 181 lseagfvctgkdvqvcfcscgcccgmweeddpmkemhampcceflrskkseetqyi 240  
 241 QSYVGFVDITGEHFVNSWVQRELPMASAYCNSIFAYEELRLDSKDKMPRESAVGVALA 300  
 241 qsyvgfvdtgehfvnswvqrelpmasaycnsifayeelrldsdkdkmpresavgvala 300  
 301 KACLFETGIDIVQCFSCGCCGCKMWEEDDPMDLDDHTRCFPNCPFLQNNKSSAEVTPLOS 360  
 301 kaclfetgidivqcfscgcccgmweeddpmdlddhtrcfpncpflqnnkssaevtplos 360  
 361 RGLCELLETTSESNLSDSIAGPIVPEMAGQEAQWFEAKNLNEQLRAAYTSASFRHMS 420  
 361 rgclcelletteesnlsdsiagpivpemagqeaqwfeknlnleqlraaytsasfrhms 420  
 421 LDISSDLATDHLGCDLSISKSHSKVQEPVLPEVFGNLSVMCVEGEASGKTVLL 480  
 421 ldissslatdhlgcdlsiskshskvqepvlpevfgnlsvmcvegeasgktvll 480  
 481 KKIATLMSGCCPLNRPOLVFYLSLSTRPDGLASITCDOLLEKESVTECMKRNIIQ 540  
 481 kkiatlmsgccplnrfpolvfylslstrpdglasitcdollekesvtecmkrniiq 540  
 541 QLNQOVFLLDLDYKEICISFOYIGKLIQKHNLSRTCLLAVRTNARDIRYLETLEIK 600  
 541 qlnqovflldldykeicisfoyigkqliqkhnlsrtcllaVRTNARDIRyletleik 600  
 601 AAFPYNTVCLTRKLFSGNNMTRLRKFNVYFGKQNSLOKIQKPLFVAALCAHMFQYPPDPS 660  
 601 aafpyntvcltrklfsgnnmtrlrkfnvyfgkqnslokiqkplfvaalcahmfqyppdps 660  
 661 FDDVAVFKSYMERLSLRNKATAEILKATVSSGEGALAKGFSSCFERNDDDLAAGVDED 720  
 661 fddvavfkymerslrrnkataeilkatvssgegalakgfsscferrnddllaagvded 720  
 721 EDLJWOLMKKFAOQLRPPRYRFLSPAFQEFLAGMRITELDSDQEHODGLYHLQINS 780  
 721 edljwolkkfaoqlrppryrflspafqeflagmritelddsdqehodglyhlqins 780  
 781 PMMTVASAVNNFLNYSVSPSTKAGPKTVSHLLVYDNKESLENISENDYLYKHQPEISIQ 840  
 PMMTVASAVNNFLNYSVSPSTKAGPKTVSHLLVYDNKESLENISENDYLYKHQPEISIQ 840

Db 781 pmmtvasavnnflnyvs]pstkagpkivshllhlydnkeslensendylykhqpeis]q 840  
 QY 841 MOLLRLGMOICPOAYFSWSEHLLVATLKTAVQNSMTVAACSPFYOLPQGTTLTGALNT 900  
 Db 841 mllrlglmoicpoyfswsehlhvlatlktavqnsmtvaacspfyolpqtltlgaln 900  
 QY 901 QYFDPRESLSLRSHHPFRGNKTSPPRAHNSVLETCEDKNSQVPTIPQDYASAFEPNNEW 960  
 Db 901 qyfdpreslslrshhpfrgnktspprahnsvleetcedknsqvptipodyasafepnnew 960  
 QY 961 ENRLAEKEDNVASYWDMQRRASPDLSGYWKLSPKQYKIPCLFVDVNDIDVYQDMLETL 1020  
 Db 961 enrlaekednvasywdmqrraspdls gywklspkqyk ipclfvdvndidvyqdmle 1020  
 QY 1021 MTFVSASORIELHNSRGFESTIRPALLESKASVTKCSISKLSLADEQLLTLPSLE 1080  
 Db 1021 mtfvsasorielhnsrgfestirpalleskasvtkcsiskls la deqltltpsle 1080  
 QY 1081 SLEVSGTIOGODOIFPNLXKFLCKELSYDLKCNINVFVYIPEEPNFMHMKLTIOTISA 1140  
 Db 1081 slevsgtiogodofpnlxkflckelsydlkcninvfvyipeepnfmmhmkltiotisa 1140  
 QY 1141 EYDPSKLVKLIQNSPMLHVFHLKCNFSDFGSLMTWLVCKRLTLTKSDSFQAVPEVA 1200  
 Db 1141 eydpskvlvqliqnsplhvfhlkcnfsgdsglmtwlvckrltltkdsdfqavpeva 1200  
 QY 1201 SLPNFISLKLNLNEGOFDPDEETSEKFAVILGSLSNBELILPDCGIVRYAKLIIQCCQ 1260  
 Db 1201 slpnfislklnlnegofdpdeetsekfavilgslsnbelilpdcgivyryakliiqccq 1260  
 QY 1261 QLHCLVLSFFRTLNDSDVYEIAKVAISGFOKLEJNLKLSINHKTDEGRANFEOALDNM 1320  
 Db 1261 qlhclvlsffrtlndsdvyeiakvaisgfoklejnlklsinhktdegranf eoal 1320  
 QY 1321 PMLOELDSRHFTPECIRKQATTVKSLSGCVLRDLRLNMLSWLADADIALANPKER 1380  
 Db 1321 pmlodeldsrhftpecirkqatvkslsgcvlrldrlnmlswladadialanpk 1380  
 QY 1381 HPOSKYLTILQKWLIPESPIIQ 1403  
 Db 1381 hpqskyltcllqkwllpfspilqk 1403

RESULT 4  
 ID AAY88053 standard: Protein: 1403 AA.  
 AC AAY88053:  
 DT 22-SEP-2000 (first entry)  
 DE Human NAIP protein.  
 XX  
 KW NAIP; apoptosis inhibiting protein; monoclonal antibody; diagnosis;  
 KW apoptosis disease onset mechanism; drugs development; prevention;  
 KW treatment; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH key Location/Qualifiers  
 FT Region 256..586  
 FT /note="Immunogenic region, specifically described  
 FT Region 841..1052  
 FT /note="Immunogenic region, specifically described  
 FT /note="In Claim 1"  
 PN W0200024889-A1.  
 XX  
 PD 04-MAY-2000.  
 XX  
 PF 22-OCT-1999; 99WO-JP05841.  
 XX





OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 600 /note= "encoded by AAA"  
FT Misc-difference 919 /note= "encoded by AAA"  
FT /note= "encoded by CCA"  
XX  
XX MO9726331-A2.  
XX  
XX 24-JUL-1997.  
XX  
XX 17-JAN-1997: 97MO-IB00142.  
XX  
XX 19-JAN-1996: 96GB-0001108.  
XX  
XX (UYOT-) UNIV OTTAWA.  
XX  
XX Korneluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K;  
PI  
DR WPI: 1997-385335/35.  
DR N-PSDB: AAT71266.  
XX  
XX  
XX New neuronal inhibitor of apoptosis - useful for diagnosing and  
PT treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis  
XX  
XX Clatm 41; Fig 7A-L; 102pp; English.  
XX  
XX Novel human neuronal apoptosis inhibitor protein (AAM20033), or NAIP,  
CC is a negative regulator of apoptosis, partic. neuronal apoptosis  
CC and, when deficient or absent, contributes to neurodegenerative  
CC phenotypes such as spinal muscular atrophy (SMA) and amyotrophic  
CC lateral sclerosis. Its amino acid sequence was deduced from a  
CC cDNA clone (AAT71266) obtd. from a human foetal spinal cord cDNA  
CC library. NAIP polypeptides, esp. those containing at least two  
CC BIR (baculovirus IAP repeat) domains, can be expressed in host-  
CC vector systems and used to increase or induce apoptosis in host-  
CC treatment of AIDS, neurodegenerative disease, myelodysplastic  
CC syndromes or ischaemic injury, to screen for (anti-)agonists, or to  
CC produce antibodies useful for inhibiting apoptosis.  
XX  
XX Sequence 1403 AA:

Query Match 99.7%: Score 7284; DB 18; Length 1403;  
Best Local Similarity 99.7%: Pred. No. 0;  
Matches 1399: Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MATQOKASDERISQFDHNLPELSALLGLDPAVOLAKLEEEERAKKQKGNQMSQSE 60  
DB 1 matqkasderisqfhdnlpeelsallglidavglakeleeeekeraakmgkynsqmzse 60  
QY 61 AKRLKTFVTEBPYSSWIPQMAAAGFTGCVKSGIOCFCCSLILFGAGLTRPIEDHKRF 120  
DB 61 akrlktfvtebpyswipqmaaaagftgcvksigcfcscslilfgagltrpiedhkrf 120  
QY 121 HPDCCFLNKNVGNIAKYDIRVKNLSRLRGCMRYQEEEARLASFRNPFVQGISQCV 180  
DB 121 hpdccflnknvgniakydirvknlsrlrgcmryqeeearlasfrnpfvqgisqcv 180  
QY 121 hpdccflnknvgniakydirvknlsrlrgcmryqeeearlasfrnpfvqgisqcv 180  
DB 121 hpdccflnknvgniakydirvknlsrlrgcmryqeeearlasfrnpfvqgisqcv 180  
QY 181 LSPAGFVETCKQOTVCCFSCGCGGLGMEEGDDPMKEMKPFCKFLSKSKSSEETIYI 240  
DB 181 lspagfvctkqotvccfscgcgglgmeegddpmkemkpfckflsksksseetiyl 240  
QY 241 QSYKGFVDITGEHFNVMQRELPMASAVCNDISFAYEELRLDSKMDPRSAVGAALA 300  
DB 241 qsykgfvdtgehfvmqrelpmasavcndisfayeelrldskmprsaavgaaala 300  
QY 301 KAGLEPTGKIDLVQCFSCGCGGLEKQEGDDPLDHTRCFPMCPLOMKNKSSAEVTPDLS 360  
DB 301 kagleptgkidlvcfscgcgglekqegddpldhtrcfpmcplomknkssaevtplds 360  
QY 361 RQELCELLETSESNTLEDSIAVGPVPEMAGCEAQMFOEAKNINLEQLAAATYSASFRHMS 420

DB 361 rgeclcellettsesnledsiavgpivpemaggeqwfqeaqnlnleqlraatysasfrhms 420  
QY 421 LLDISSDLATBMLCCDLSIASKSHISKPOEPLVLEFGNLSNMGVEGAGSGKTVLL 480  
DB 421 lldissdlatbmlccdlslaskshiskpoeplvlefgnlsnmgvegagsgktvll 480  
QY 481 KKIATLMAAGCCPLNRFQVFLSYLSSTRPDEBLASICDOLLEKGSVTENCMRNIIQ 540  
DB 481 kkiatlmaagccplnrfqvfslsystrpdeblasicdollekgsvtencmrniiq 540  
QY 541 OLKNOVFLDDYKEIGSIPQVIGKLQKKNHLSRTCLLIAPFRNARDIRRYETLEIK 600  
DB 541 olknovfllddykeigsipqvigklqkknhlsrtclliapfrnardirryetleik 600  
QY 601 AFPEYNTVCILRKLEFSHNMRKRFMYFEKKNOSLOKIQKTPLEVAALCAHMFQYFPDS 660  
DB 601 afpeyntvcilrklefshnmrkrfmyfekknoslokioqktplevalcahmfqyfpds 660  
QY 661 FDDVAVERKSYMERLSLNKATAEILKATVSSGCEALAKGFCSCFPFNDDLAEGVDED 720  
DB 661 fddvaverksymerlslnkataelkatvssgcealakgfcscfpfnddlaegvded 720  
QY 721 EDLTMCIMSKFTQRLRPFRFISPAFOEFLAGMRLIEDLSDROEHODLGLYHLKQINS 780  
DB 721 edltmcimskftqrlrpfrrfispafoeflagmrlie dlsdroehodlgllyhlkqins 780  
QY 781 PMKTVASAYNNFLNYSVLSPTKAGPKIVSHLHLVDNKNSELENISENDYLRKHOPEISLQ 840  
DB 781 pmktvasaynnflnysvlsptkagpkivshlhlvdnknse lenisendylyrkhopeislg 840  
QY 841 MQLRLQMICQAVFSMSSEHLLVLAALKTAVQSNFVAASPFVLOPLQGTTLTGALNL 900  
DB 841 mqlrlqmicqavfmssehlvlalalktavqsnfvaaspfvlopplqgttltgalnl 900  
QY 901 QTFPHDESLSLRSHIPRIRGNKTSPPRAHPSVLETCDSQOVTPIDODVSAEPENMEW 960  
DB 901 qtfphdeslslrshiprirgnktspprahpsvle tcdsqovtpidodvsae penmew 960  
QY 961 ERNLAEKEDNYSYMDMRRASPDLSITGYWKLSPKQYKIPCLEVDVNDIVVQGMLEIL 1020  
DB 961 ernlaekednysymdmrraspdlsitgywklspkqyk i pclevdvndivvqgmleil 1020  
QY 1021 MTFVASQRIELHUNHSGFTESIRPALESKASVTGCSITKLESADEBLTLTPSLE 1080  
DB 1021 mtfvasqrielhunhsgftesirpaleskasvtgcs itkle sa deb ltltpsl e 1080  
QY 1081 SLEVSQTRGOSDOIFPNIDKFLCKELISVDLEGNINVSVIPPEFPHHMEKTLIQISA 1140  
DB 1081 slevsqtrgosdoifpnidkflckel isvdle gninvsvippefphhme ktl iqisa 1140  
QY 1141 EYDPSKLVKLIONSPLHAFHLKCNFSDGSLMTMYSCKTLTELKFSDFQOAVPVA 1200  
DB 1141 eydpsklvklionsplhahfhlkcnfsgslmtmy scktl telkfsdfqoavpva 1200  
QY 1201 SLNPFISLKLINLEGOQFPDEETSEKPAVILGSLMJEELIPTGDIYRVAKLIIQOCQ 1260  
DB 1201 slnpfisllklle goqfpdeetse kpa vilgslmjeeliptgd iyrvakl iiqocq 1260  
QY 1261 QLHCLRLVSEFFKTLNDSVVEIKVAISGGFOKLEMLKSTINHKITTEBGRNPFQALDMM 1320  
DB 1261 qlhclrlvseffk tln dsvveikva isggfo klem l kst in hkitte bgrn p f qal dmm 1320  
QY 1321 PNLQELDISRHFECKKAQATTVKLSISQCVLRPLIRLMLSWLLDADDDIALINVMKR 1380  
DB 1321 pnlqeldisrhfeckkaqat tvklsisqcvlrplir lmlswll dadd ial in vmkr 1380  
QY 1381 HPOSKYLTILQKWIILPFSPPIQK 1403  
DB 1381 hposky ltilqkw iilpfsp piqk 1403  
RESULT 6

AA14080  
ID AA14080 standard; Protein; 1295 AA.  
XX  
AC AA14080;  
XX  
DT 20-JUL-1999 (first entry)  
XX  
DE Gonadotropic hormone protein sequence.  
XX  
XX Gonadotropic hormone; excessive ovulation animal; transgenic animal;  
KM totipotent cell; somatic cell chromosome.  
XX  
OS Homo sapiens.  
XX JP1113444-A.  
XX  
PD 27-APR-1999.  
XX  
PF 14-OCT-1997; 97JP-0280830.  
XX  
PR 14-OCT-1997; 97JP-0280830.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
PA (SAKA/) SAKAI H.  
DR WPI: 1999-320709/27.  
XX N-PSDB: AAX58001.  
PT An excessive ovulation animal - useful for improving the  
PT productivity of animals  
XX  
PS Claim 3; Page 14-18; 18pp; Japanese.  
XX  
XX This sequence represents a gonadotropic hormone.  
CC The invention relates to an excessive ovulation animal, which is a  
CC transgenic animal with a totipotent cell containing a DNA fragment  
CC containing a promoter sequence and a gonadotropic hormone coding  
CC sequence. The DNA fragment is in the somatic cell chromosome. The  
CC excessive ovulation animal is useful for improving the productivity of  
CC animals. The method can improve the productivity of a useful animal.  
XX  
SQ Sequence 1295 AA;  
  
Query Match 91.6%; Score 6691; DB 20; Length 1295;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1282; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 NATQOKASDERISQFDHNLPELSALGLDAVOLAKELSEEBOKERAKMKGYSQMRSE 60  
DB |||||  
1 matqkaderisqfdhnlpe lsal gl davalakel seebokera kmkgysqmrse 60  
QY 61 AKRLTFVYTERYSWIRPOEMAAGFTYGVKSGIQCFCCSLIFGAGLTRLPIDHKEF 120  
DB |||||  
61 akr ltfv yter yswir poema agf tygv ksg iqcf ccsl ifga gl trlp idh krf 120  
QY 61 akr ltfv yter yswir poema agf tygv ksg iqcf ccsl ifga gl trlp idh krf 120  
DB |||||  
61 akr ltfv yter yswir poema agf tygv ksg iqcf ccsl ifga gl trlp idh krf 120  
QY 121 HPDGFELNKKDGNIAKVDIRYKRLKSRIRGKMROEERAEALASRNMPEYVOGSPCV 180  
DB |||||  
121 hpd gfel nkkd gni akv dir ykrl ksr irg kmr oe eae ala sr nmpe yvo gsp cv 180  
QY 121 hpd gfel nkkd gni akv dir ykrl ksr irg kmr oe eae ala sr nmpe yvo gsp cv 180  
DB |||||  
121 hpd gfel nkkd gni akv dir ykrl ksr irg kmr oe eae ala sr nmpe yvo gsp cv 180  
QY 181 LSEAGFVFTGKODVQCFSCGCLGNWEEGDPMKEHAKMFKCEFLRSKSSSEETQYT 240  
DB |||||  
181 lse agfv ftgk odv qcf scgc lgn wee gdp mke h ak mfk ce fl rsk ss se etq yt 240  
QY 181 lse agfv ftgk odv qcf scgc lgn wee gdp mke h ak mfk ce fl rsk ss se etq yt 240  
DB |||||  
181 lse agfv ftgk odv qcf scgc lgn wee gdp mke h ak mfk ce fl rsk ss se etq yt 240  
QY 241 OSYKGFVDITGEHFNYSWVQRELPMASAYCNDISFAYEELRLDSFKMPRESAVGAA 300  
DB |||||  
241 os yk gf vdi tge h fn ysw vq rel pma say cnd isf ay ee lrl ds fkm p re sav gaa 300  
QY 241 os yk gf vdi tge h fn ysw vq rel pma say cnd isf ay ee lrl ds fkm p re sav gaa 300  
DB |||||  
241 os yk gf vdi tge h fn ysw vq rel pma say cnd isf ay ee lrl ds fkm p re sav gaa 300  
QY 301 KAGLFYTGKDI VQCFSCGCLGKMOEGDDPLDHRCPNCPFLONMSSAEVPPDOS 360  
DB |||||  
301 kag lfy tgd i vqc fscgc l gk mo eg ddp l dhr c pnc pfl on mss ae vpp dos 360  
QY 301 kag lfy tgd i vqc fscgc l gk mo eg ddp l dhr c pnc pfl on mss ae vpp dos 360  
DB |||||  
301 kag lfy tgd i vqc fscgc l gk mo eg ddp l dhr c pnc pfl on mss ae vpp dos 360  
QY 361 RGLCELLETTSSENLSDIAVGPIVPEMAQCEAGWFCRAKKNLEQLRAAYTSASPRHMS 420  
DB |||||  
361 rgl cel let ts sen lsd iavg piv pe ma qce agw fcr ak kn le ql ra ay ts as pr hms 420

DB |||||  
361 rgl cel let ts sen lsd iavg piv pe ma qce agw fcr ak kn le ql ra ay ts as pr hms 420  
QY 421 LLDISSDLATBHLGCDUSIASKHISKPYOEPLVPEVFGNINSWCVEGEGSGKTVLL 480  
DB |||||  
421 lld iss dlat bhl gcd us iask h isk py oe pl vpe vfg nins wc ve geg sgk tv ll 480  
QY 421 lld iss dlat bhl gcd us iask h isk py oe pl vpe vfg nins wc ve geg sgk tv ll 480  
DB |||||  
421 lld iss dlat bhl gcd us iask h isk py oe pl vpe vfg nins wc ve geg sgk tv ll 480  
QY 481 KRIATFLMAGCCPPLNRPOLVFLSLSTRPREGLASITCDQLLEKESVTEMCNRNIO 540  
DB |||||  
481 kri at fl ma gcc ppl nr po lv fl sl str pre gla sit cd ql le kes vte mcn rn io 540  
QY 481 kri at fl ma gcc ppl nr po lv fl sl str pre gla sit cd ql le kes vte mcn rn io 540  
DB |||||  
481 kri at fl ma gcc ppl nr po lv fl sl str pre gla sit cd ql le kes vte mcn rn io 540  
QY 541 OLKNQVFLFLDDYKEICSPQYIGKLIQKNHLSRPTCLIAVTRNARDRRLLETLERIK 600  
DB |||||  
541 ol knqv fl fl ddy ke ic sp qy ig k li qkn h ls rpt cl iav tr nar dr rll e tl er ik 600  
QY 541 ol knqv fl fl ddy ke ic sp qy ig k li qkn h ls rpt cl iav tr nar dr rll e tl er ik 600  
DB |||||  
541 ol knqv fl fl ddy ke ic sp qy ig k li qkn h ls rpt cl iav tr nar dr rll e tl er ik 600  
QY 601 AFPEYNTVCILRKLPESHNTLRKRFVYFGKNQSLQIKOTPLFYAALICAHMPQYPPDS 660  
DB |||||  
601 af pe ynt vc il rk lp esh nt lr k rf v yfg kn qsl q i k ot pl fy aa li ca h mp qy pp ds 660  
QY 601 af pe ynt vc il rk lp esh nt lr k rf v yfg kn qsl q i k ot pl fy aa li ca h mp qy pp ds 660  
DB |||||  
601 af pe ynt vc il rk lp esh nt lr k rf v yfg kn qsl q i k ot pl fy aa li ca h mp qy pp ds 660  
QY 661 FDDVAVFKSYMERLSIRNKATAEILKATVSCGELALKGFCSCPEFNDDILAEGVDED 720  
DB |||||  
661 fdd vav fks ymer ls ir nk at ae il ka tv sc ge la l kg fsc cpe fn dd ila eg v ded 720  
QY 661 fdd vav fks ymer ls ir nk at ae il ka tv sc ge la l kg fsc cpe fn dd ila eg v ded 720  
DB |||||  
661 fdd vav fks ymer ls ir nk at ae il ka tv sc ge la l kg fsc cpe fn dd ila eg v ded 720  
QY 721 EDLTMCIMSKPTAORLPFRFLSPAQEFELAGMRLEILDSRQEHODLGLYHLKOINS 780  
DB |||||  
721 ed lt mc im sk pt aor l pfr fl spa qef el ag mr le il ds r q eh od l gl yhl ko ins 780  
QY 721 ed lt mc im sk pt aor l pfr fl spa qef el ag mr le il ds r q eh od l gl yhl ko ins 780  
DB |||||  
721 ed lt mc im sk pt aor l pfr fl spa qef el ag mr le il ds r q eh od l gl yhl ko ins 780  
QY 781 PMKTVSATNPNFNYVSSLPSTKAGPKYVSHLHLVDNKESENISENDYLRKQEPISQ 840  
DB |||||  
781 pm ktv sat n pnf ny vss l pst ka g pk yv sh l hl vdn ke sen ise ndy lr k qe pis q 840  
QY 781 pm ktv sat n pnf ny vss l pst ka g pk yv sh l hl vdn ke sen ise ndy lr k qe pis q 840  
DB |||||  
781 pm ktv sat n pnf ny vss l pst ka g pk yv sh l hl vdn ke sen ise ndy lr k qe pis q 840  
QY 841 MQLRLGIMQICPOAFVSMVSEHLVLAKTAVQSNMVAACSPFVQFLGRLTLGALNL 900  
DB |||||  
841 mql rlg im qic po af vsm vseh lv la kt av qsn mva ac sp fv ql gr ltl gal nl 900  
QY 841 mql rlg im qic po af vsm vseh lv la kt av qsn mva ac sp fv ql gr ltl gal nl 900  
DB |||||  
841 mql rlg im qic po af vsm vseh lv la kt av qsn mva ac sp fv ql gr ltl gal nl 900  
QY 901 QYFFDHPESLSLRSIHPRIRGNKTSPPRAHFSVLETCPDKSOVPTIDOPYASAFEPNEM 960  
DB |||||  
901 qy ffd h pes ls lrs ih pr ir gn kts pp rah fs vlet cp dk so vpt id op ya sa fe pn em 960  
QY 901 qy ffd h pes ls lrs ih pr ir gn kts pp rah fs vlet cp dk so vpt id op ya sa fe pn em 960  
DB |||||  
901 qy ffd h pes ls lrs ih pr ir gn kts pp rah fs vlet cp dk so vpt id op ya sa fe pn em 960  
QY 961 EBNLAKEEDNVKSYNDMORASPDLSGTWKLSPKQYKIPCLVDYNDIDVYGQMLETL 1020  
DB |||||  
961 ebn la ke ed nv ksy nd mo ras p dls gt wk l sp k qy k ip cl vdy nd id vy gq m le tl 1020  
QY 961 ebn la ke ed nv ksy nd mo ras p dls gt wk l sp k qy k ip cl vdy nd id vy gq m le tl 1020  
DB |||||  
961 ebn la ke ed nv ksy nd mo ras p dls gt wk l sp k qy k ip cl vdy nd id vy gq m le tl 1020  
QY 1021 MTFVSAQRIEHLNRSRFEISIRPALSKASVYKCSISKLELSAABOEILLTPSIE 1080  
DB |||||  
1021 mtf vsa qrie hln rsr f eis ir pal sk as v yk cs is k le ls aab oe ill tp sie 1080  
QY 1021 mtf vsa qrie hln rsr f eis ir pal sk as v yk cs is k le ls aab oe ill tp sie 1080  
DB |||||  
1021 mtf vsa qrie hln rsr f eis ir pal sk as v yk cs is k le ls aab oe ill tp sie 1080  
QY 1081 SLEVSCTIOSODIIFPNLDKFLCLKELSYDLBGNINVFPSVIRPEEPFNHMEKLLIQISA 1140  
DB |||||  
1081 sle vs ct ios o di if pn ld k fl cl kel sy dl bgn in vf ps vir pe ep fn h me k ll iq isa 1140  
QY 1081 sle vs ct ios o di if pn ld k fl cl kel sy dl bgn in vf ps vir pe ep fn h me k ll iq isa 1140  
DB |||||  
1081 sle vs ct ios o di if pn ld k fl cl kel sy dl bgn in vf ps vir pe ep fn h me k ll iq isa 1140  
QY 1141 EYDPSKLVKLIONSPMLHFNHLKCNFSPGSLMTMLVSCKLTLEKESDFFQAVPFA 1200  
DB |||||  
1141 ey d ps k lv kl ion sp ml h fn hl k cn fsp g sl mt ml vsc k lt le kes dff q av p fa 1200  
QY 1141 ey d ps k lv kl ion sp ml h fn hl k cn fsp g sl mt ml vsc k lt le kes dff q av p fa 1200  
DB |||||  
1141 ey d ps k lv kl ion sp ml h fn hl k cn fsp g sl mt ml vsc k lt le kes dff q av p fa 1200  
QY 1201 SLPNFSLKTLNLEGOQPDDEETSEKFAVILISLSLLEELIPTGGYIRVAKLLIQOCO 1260  
DB |||||  
1201 sl pnf sl k tl n le go qpd de et se k fa vil is ls l le el ipt gg yir v ak ll iq oco 1260  
QY 1201 sl pnf sl k tl n le go qpd de et se k fa vil is ls l le el ipt gg yir v ak ll iq oco 1260  
DB |||||  
1201 sl pnf sl k tl n le go qpd de et se k fa vil is ls l le el ipt gg yir v ak ll iq oco 1260  
QY 1261 QLHCLRLVLSFFFTLNDSSVEEIAKV 1285  
DB |||||  
1261 ql h cl rlv ls fft lnd ssv ee iak v 1285  
QY 1261 ql h cl rlv ls fft lnd ssv ee iak v 1285  
DB |||||  
1261 ql h cl rlv ls fft lnd ssv ee iak v 1285  
  
RESULT 7  
AA09540  
ID AA09540 standard; Protein; 1295 AA.  
XX  
AC AA09540;  
XX  
DT 20-JUL-1999 (first entry)  
XX  
XX Human apoptosis inhibiting protein #2.

XX Human: apoptosis inhibitory protein; apoptotic disease; diagnosis;  
 KW spinal muscular atrophy.  
 OS Homo sapiens.  
 XX JP11116599-A.  
 XX 27-APR-1999.  
 XX 14-OCT-1997; 97JP-0280831.  
 XX 14-OCT-1997; 97JP-0280831.  
 XX 14-OCT-1997; 97JP-0280831.  
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX WPI: 1999-323531/27.  
 XX N-PSDB; AAX56273.  
 XX New apoptosis inhibitory protein - useful for determining mechanism  
 PT of various apoptotic diseases e.g. human spinal muscular atrophy  
 PS Claim 1: Page 8-11; 16pp; Japanese.  
 XX The present sequence represents a human apoptosis inhibitory protein.  
 CC The apoptosis inhibitory protein is useful for the elucidation of  
 CC the mechanism of various apoptotic diseases such as human spinal  
 CC muscular atrophy and the diagnosis, the prevention and the treatment  
 CC of such diseases.  
 XX Sequence 1295 AA;  
 SO  
 Query Match 91.6%; Score 6691; DB 20; Length 1295;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1282; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 541 QLNQVLFLLDDYKEICSIPOVIGKIQKHLSTRCLLIIVRTNRARDIRRYETLEIK 600  
 DB 541 qlknqylfllddykelcetsipvgklqknhlstrclliavtrnrardirryetleik 600  
 OY 601 APFFYNTWCILARKLFSSHMTLRKRFMYVFGKNSIQKIQKTPLEVAICAHMFQPPDPS 600  
 DB 601 afpfyntwcilarklfsshmtlrkrfmyvfgknsiqkiktplevalcahmfqppdps 600  
 OY 661 FDDVAVFKSYMERSILRNKATAEILKKNVSCGLAKGFFSCCFEPNDDLAEGVDSD 720  
 DB 661 fddvavfksymersilrnkataelkknvscglakgffscfepnddlaegvdsd 720  
 OY 721 EDLTGCLMSKFTARLRPFYRFLSPAFQEFACMRLELSDSDROHQDLGYHLKQIMS 780  
 DB 721 edltgclmskftarlrpfyrfllspafqefacmrlelstdsdrohqdlgyhlkqims 780  
 OY 781 PMMTVSAYNNFLVYSSSLPSTKAGPKIVSHLILVONKSELENISNDYLRHPEISLQ 840  
 DB 781 pmmtvsaynnflvyssslpstkagpkivshlilvonkseleenisndylrhpeislq 840  
 OY 841 MQLRGLOICPOAFSVMSEHLVLALKTAVQSNVAAQSPFVLQPLQGRITLIGALNL 900  
 DB 841 mqlrgloicpofsvmsehllvllalktavqsnvaaqspfvllqgritlilgalnl 900  
 OY 901 QYFDDHPESTLSLRSHFPIRGNKTSPPRAHPSVLETCFCDKSGVPTDODYASAEPMNEW 960  
 DB 901 qyfddhpestlsrshfpirgnktspprahpsvleetcfcchksgvptdodyasaeppmnew 960  
 OY 961 ERNLAEKEDNVKSYMMDKQRAQSPDLSTGYWKLSPKQYKIPCLEVDVNDIVVGDMLIEL 1020  
 DB 961 ernlaekednvksymmdkraqspdlstgywklspkykiplevdvndivvgdmliel 1020  
 OY 1021 MVEFSAQSRIELHLNHSRGFIESIRPALELSKASVTCGSIKLSLAABDELLTTPSLE 1080  
 DB 1021 mvfesaqsrielhlhnsrgfiesirpalelskavtcgsklskslaabdelldtppsle 1080  
 OY 1081 SLEVSGTIOSSODQIFPNIDKFLCLKEISVDIEGNIINFSVPIPEFPFHMEKLLIQISA 1140  
 DB 1081 slevsgtiossodqifpnidkflclkeisvdieginifsvpipefpfhmeklliqisa 1140  
 OY 1141 EYDSKLVKLLIQNSPNLHVFLKCNFSDGSLMTMLVSCCKLTELKFSDFQAVPVA 1200  
 DB 1141 eydsklvklliqnspnlhvflkcnfsgslmtmlvscckltelekfsdfqavpva 1200  
 OY 1201 SLNPFISKLINLEGOFPDEETSEKRAYILGSLSLMBELILEPTGDIYVAKLLIQOQO 1260  
 DB 1201 slnpfisklinleqgfpdeetsekfayilgslslmbelileptgdiyvaklliqoqo 1260  
 OY 1261 QLHCLRLSLSPFKTLNDSVVEIAKV 1285  
 DB 1261 qlhclrlslspfktnldssvveigel 1285  
 RESULT 8  
 AAR98217  
 ID AAR98217 standard; Protein; 1232 AA.  
 XX  
 AC AAR98217;  
 XX  
 DT 30-DEC-1996 (first entry)  
 XX  
 DE Neuronal apoptosis inhibiting protein.  
 XX  
 KW Neuronal apoptosis inhibiting protein; human; NAIP; chromosome 5q13; VAC;  
 KW yeast artificial chromosome; spinal muscular atrophy; mammalian cell;  
 KW autosomal recessive; neurodegenerative disorder; alpha motor neuron; SMA;  
 XX spinal cord; proximal voluntary muscle; therapy; apoptotic mechanism.  
 OS Homo sapiens.  
 XX W09612016-A1.  
 XX  
 XX  
 PD 25-APR-1996.

XX 17-OCT-1995: 95MO-CA00581.  
XX  
XX 19-DEC-1994: 94CA-2138425.  
PR 18-OCT-1994: 94GB-0021019.  
XX  
PA (SHKJ ) RES DEV CORP JAPAN.  
PA (UYOT-) UNIV OTTAWA.  
XX  
PI Ikeda J, Korneluk RG, Mackenzie AE, Mahadevan MS;  
PI Mclean M, Roy N;  
XX WPI: 1996-222003/22.  
DR N-PSDB: AAT30092.  
XX  
PT Neuronal apoptosis inhibitor protein gene - used to develop prods.  
PT for use in the diagnosis and therapy of spinal muscular atrophy  
XX  
XX Claim 3; Page 68-70; 113pp; English.  
XX  
XX This sequence represents the human neuronal apoptosis inhibitor protein  
XX (NAIP). The cDNA encoding this sequence was found on a region of the  
XX human chromosome 5q13. This sequence was isolated from a yeast  
XX artificial chromosome (YAC) contig containing the D5S435-D5S112 interval  
XX of the chromosome 5q13. Mutations in the NAIP gene, are causative of  
XX spinal muscular atrophy (SMA) types I, II, and III. SMAs are a group of  
XX autosomal recessive, neurodegenerative disorders. SMAs are classified  
XX into the three types based upon the age of onset (with type I being the  
XX severest form with the earliest age of onset). All three types are  
XX characterised by the degeneration of the alpha motor neurons of the  
XX spinal cord manifesting as weakness and wasting of the proximal voluntary  
XX muscles. The most common mutations of the NAIP gene sequence are thought  
XX to be deletions of exons 5 and 6, and reductions in the copy number of  
XX the gene. The NAIP gene, (and primers and probes based on it) can be  
XX used for the diagnosis of SMA, and for directing the formulation of  
XX conventional and genetic therapies for SMA. Identification of genes  
XX showing homology with the NAIP locus, and proteins that interact with  
XX NAIP can be used in the elucidation of apoptotic mechanisms in mammalian  
XX cells.  
XX  
XX Sequence 1232 AA;  
SQ

Query Match 87.2%; Score 6373.5; DB 17; Length 1232;  
Best Local Similarity 95.9%; Pred. No. 0;  
Matches 1229; Conservative 1; Mismatches 1; Indels 51; Gaps 1;

QY 1 MATQOKASDERISQFDHNLPELSALGLDAVOLAKLEEEBOKERAMQKGYNSMRSE 60  
Db 1 matqkasaderisqfdhnlpealsalgldayqlakeleeeqkeramqkgynsmrse 60  
QY 61 AKRLKFTPTTYPYPSMIFQEMAAAGFYTYGKSGIQCCSCSLIFGAGLTLPLIEDHRRF 120  
Db 61 akrkftptttypysmifqemaagfytvgksgiqccscslifgagltlpliedhrrf 120  
QY 121 HPDGGFLLNKRVGNIAKADIRVKNLKSRLRGCKMRYOEEERLASFRRMPYVOGISCV 180  
Db 121 hpdggfllnkrgvgniakdirtvknlsrllrgckmryoeearlasfrmplyvqgispcv 180  
QY 181 LSEAGFVFTGKQDVTVOCFSCGCGCLNMWEGDDPWKEHAKWPKCFELSKSSSEETIYI 240  
Db 181 lseagfvftgkqdvtfvcfscgcgclnmwegddpwkehakwfpkceflskssseetiyi 240  
QY 241 QSYTGFDYDITGEHFNVSNGVQRELPMASAYCNDSTFAYEELLDSTFKMPRESANGVAALA 300  
Db 241 qsytgfdyditgehfnvsngvqrelpmasaycndstfayeelldstfkdpresangvaala 300  
QY 301 KAGLFYTGIRKDIYOCFSGCGCLERKMQEGDDPLDHTTRCFPNCPLONKSSAEVTPDLQS 360  
Db 301 kaglfytgirkdiyocfsgcgclerkmqegddpldhttrcfpncplonkssaeetvtpdlqs 360  
QY 361 RGEICELLETTSSESINLEDSIAVGPVPEMAOGEAQWFOEAKNLNEQLRAAVTASAFRHS 420  
Db 361 rgeicellettssesinledsiavgpvpepmaogeaqwfgeaknlneqlraavtsafrhs 420

Db 361 rgeicellettssesinledsiavgpvpepmaogeaqwfgeaknlneqlraavtsafrhs 420  
QY 421 LLDISSDLATPHLGGCDLSIASKHSKRVORPVLVPEFGHNLNVMCYEGSAGSKTYLL 480  
Db 421 lldissdlatphlggcdlsiaskhskrvorpvlvpefghnlsvmcyegsagsktyll 480  
QY 481 KRIAFIMASGCCPLNRFQALFYVLSLSTRPDEGLASTIICQDLKEKESVTEMCARNIIQ 540  
Db 481 kriaflmasgccplnrfqalfyvlslstprdeglastiiicqdlkekesvtemcarniiq 540  
QY 541 QLKNOVFLLDYKEIGSIPOVIGKLQKNHLSRTCLLIAVRNARDIRRYLETIEIK 600  
Db 541 qlknovflldykeigsipovigklqknhlsrtclliavrnardirryletieik 600  
QY 601 AAPPFNVCILIRKLESHMTRLRKPMVYEGNOSLOKOKPTPLPAALCAWFOYPCPS 660  
Db 601 aappfnvcilirkleshmtrlrkpmvyegnoslokokptplpaalcawfoypcps 660  
QY 661 FDDVAVFESYMERLSLRNKATAEILKATVSSCGELALKGFFSCGFENDDDLAEGVDED 720  
Db 661 fddvavfesymerlslnrkataeilkatvsscgelalkgffscgfennddllaegvded 720  
QY 721 EDLWCLMSKFTAQRRLRPFYFLSPAFOEPLAGMKRLIELDSDROHODLGLYHLKQINS 780  
Db 721 edlwclmskftaqrllrpfyflspafoeplagmkrlieldsdrohodlgllyhlkqins 780  
QY 781 PMKTVSANNLNLYVSSLPSTRKAGKYSHLLHLYDNKNESENLESENDDYIAKHQPEISIQ 840  
Db 781 pmktvsannlnlyvsslpstrkagkyshllhlydnknelesenleSENDDYIAKHQPEISIQ 840  
QY 841 MOLLRLGLOIQPOAFVSWSEHLVLAUKTAYOSNTVAAQSPVLOFLOGRTLTGALNL 900  
Db 841 mllrlglolqpoafvswsehlvlauktayosntvaaqspvloflogrtltgalnl 900  
QY 901 QYFDPHPSLSLRSIHPRIGKNTSPRAHFSVLETCFDSQVPTIIDQIVASAEFPNNEW 960  
Db 901 qyfdphpslslsrshprigkntsprahfsvleTCFDSQVPTIIDQIVASAEFPNNEW 960  
QY 961 ERNLAEREDNYSYVMDORRASPDLSTGWTLSPRQYVILPCELVNDVNDIVGGOMLETL 1020  
Db 961 ernlaerednysyvmдорaspdlstgwtlsprqyvilpcelvndvndivggomleTL 1020  
QY 1021 MTFVSASORIELNLNHSRGFTIESIRPALELSKASVTKCSISKLELSAAEQELLTLPSLE 1080  
Db 1021 mtvfasorielnlNHSRGFTIESIRPALELSKASVTKCSISKLELSAAEQELLTLPSLE 1080  
QY 1081 SLEVSCTIOSODQIFPNLDKFLCLKELSVDLGGINVFSVIPDEEFPNFHMEKLLIQISA 1140  
Db 1081 slevsctiosodqifpnldkflclkelSVDLGGINVFSVIPDEEFPNFHMEKLLIQISA 1140  
QY 1141 EYDPSKLYKLONSPNLHVPFLKCNFPDPSLMTMLVSCAKLREIKSDSFPQAVPPVA 1200  
Db 1141 eydpsklyklonspnlhvpflkcnfpdpslmtmlvscaklreIKSDSFPQAVPPVA 1200  
QY 1201 SLNPFSLKILNLLEGQOPDEETSEKPAYILGSLNLEELILPBGDGIYRAKLLIQOCO 1260  
Db 1201 slnpfslklnllegqopdeetsekpayilgslNLEELILPBGDGIYRAKLLIQOCO 1260  
QY 1261 QLHCLRLVSFFKTLNDSVVEI 1282  
Db 1210 qlhclrlvsffkTLNDSVVEI 1231

RESULT 9  
AAU02881  
ID AAU02881 standard; Protein: 1204 AA.  
XX  
XX AAU02881:  
AC  
XX  
XX 12-SEP-2001 (first entry)  
DT  
XX  
XX Human caspase recruitment domain 12 (CARD-12) polypeptide #2.  
DE  
XX

KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
 KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
 KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
 KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
 KW aplastic anaemia; myocardioid infection; inflammatory disorder;  
 KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
 KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
 KW tuberculosis; ischaemic brain injury; hypoxic brain injury;  
 KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
 KW excitotoxic brain damage; liver disease.  
 XX Homo sapiens.  
 XX  
 XX MO200130971-A2.  
 XX  
 XX 03-MAY-2001.  
 PD  
 XX 26-OCT-2000: 2000MO-US29643.  
 PF  
 XX 27-OCT-1999: 99US-0161822.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Bertin J, Robison KE;  
 PI  
 XX WPI: 2001-308628/32.  
 DR  
 XX N-PSDB: AAS03946.  
 XX  
 PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
 PT encoding them, useful for treating and diagnosing disorders associated  
 PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
 PT disease.  
 XX  
 XX Disclosure: Fig 2; 93pp; English.  
 PS  
 XX  
 XX The sequence represents a human caspase recruitment domain 12 (CARD-12)  
 CC polypeptide. CARD domains are found in a number of proteins that transmit  
 CC signals that activate apoptosis and inflammatory pathways in response to  
 CC stress and other stimuli. Therefore, CARD-12 and its corresponding  
 CC nucleic acid may be used in treatment and diagnosis of patients suffering  
 CC from disorders associated with an abnormal level (an increase or a  
 CC decrease) of apoptotic cell death or abnormal activity of stress-related  
 CC pathways. The disorders include cancer, viral infections (e.g. caused by  
 CC poxviruses, adenoviruses), autoimmune disorders (e.g. systemic lupus  
 CC erythematosus, arthritis), neurological disorders (e.g. Alzheimer's  
 CC disease, amyotrophic lateral sclerosis), haematologic diseases (e.g.  
 CC aplastic anaemia, myocardioid infection, stroke), inflammatory and  
 CC system disorders (e.g. Crohn's disease, insulin-dependent diabetes,  
 CC contact dermatitis, psoriasis, graft rejection), bacterial infections  
 CC (e.g. tuberculosis, lepromatous leprosy), ischaemic and hypoxic brain  
 CC injury, kidney ischaemia/reperfusion injury, excitotoxic brain damage,  
 CC acute bacterial meningitis and liver disease.  
 CC  
 CC  
 XX  
 SQ Sequence 1204 AA:  
 Query Match 9.0%; Score 661; DB 22; Length 1204;  
 Best Local Similarity 23.0%; Pred. No. 5.3e-46;  
 Matches 280; Conservative 211; Mismatches 444; Indels 284; Gaps 48;  
 OY 272 DSIFAY-----BELRLDSFKMPRESAVGA-ALAKAG-----LFYTGIRDIYVCFSCGG 320  
 DB 164 ddlfwmvlnreavnlccevqdgdaargllhmllkksaesclfklskne----- 214  
 OY 321 CLEKMOEGDDPLDHTRCFPCNCFQNMK-SSAEVTPD-----LQSRGLCELETTSESNTL 376  
 DB 215 -----W-----nylfgldngsfecelqmwffnltsslglfngtsegl 225  
 OY 377 EDSIAVGIVPEMAGGEQMFQEAKNLNEODLRAAYTSASFRHNSLDDISSDLATDHLGCG 436  
 DB 256 dd-----LagdkldyhtpsfInf-----ypIge 279  
 OY 437 DLST---ASKHISKPV-----QEPVLVPEVFGNLSVNCVCEGAGSGRTVLKKRI 483

DB 280 ddlfmlksetfevrlwrkdqnhhrveqllngllqalspccliesgskyscllgrt 339  
 OY 484 AFLMAGCCPLNRLQFLYLSLSTRPDEGLASITDOLLEKGVSTEMCNIIQOLK 543  
 DB 340 amlwsgyckelktfkfvtflrtis--raagllfctcdqllldiptrktctfmaamlkr 397  
 OY 544 NOYFLDDYKEITSIQO---VIGKLQKNHLSRTCLLVNFRNRARDIRYETLEK 600  
 DB 398 qvllildgynef--kqncpeleallkenhrfkmmvlttceclrtlrfgalaevg 455  
 OY 601 AFPEYNTVCILRLKFSHNMRLKFMVYFGKNOSLOKIQKTPLEVAALCAHMYOYPPDS 660  
 DB 456 dmedesagallirevllkela--egllqkqkrcrlnlnkkrlfvltcalqmgseefhs 513  
 OY 661 FDDVAVFKSYMERLSLRN-----ATAELKATVSSGCELAKCFSCCFENDDLAE 714  
 DB 514 hqgtclhtfydlilqknkhkkgvaasdfir-sldhgdlalegvfshkldfclqdv-- 570  
 OY 715 AGVDEDEDLTMCLMSKFTQORLRPFRLSPAPQFLAGMLRIELDSDROEHODLGLYH 774  
 DB 571 ssvnedvllltgllckytatqrftkpykfthksfgytagrtlsllthhepeevtkngy 630  
 OY 775 LKQINSPMVTSAYNFNLYV--SSLPTKAGPKIVSHLHLVON----- 817  
 DB 631 lqkmvasldstlsyalllrytcgssveatra--vmkhlaayqngcllglsakrplwr 687  
 OY 818 KESLENISENDYLYKHOPEISLOMQLGLMOICQAVFSVNSHLLVLAKTVAQOST- 876  
 DB 688 gselqsvkn-----tegeellkal---nlnsfvcgihl-----ygesta 724  
 OY 877 VVACSPFVLOFQGRTRLGLALNL-OYFFDHPESLSLRSHFIRGNKTSPPRAHSYLE 935  
 DB 725 ksalsqefeaftqgkslylnsgnlpdyldf-----fienbr 760  
 OY 936 TCFDKSQVPTIDQOYASAFEPNMENENLKEEDNVKSYMDMORRASPDIStGYKLSRK 995  
 DB 761 nc--asaldlkldfygg--amaawe-----kaedtyglhmeape 798  
 OY 996 QYKPT-----CLEVDVNDIDVGOQMEILMTVFSAORTEHLNHSRPF 1040  
 DB 799 ty-lpsravsllfwmkqefrtlevtrldfeklqkdlrygklfsasatsrlrlqikcagv 857  
 OY 1041 IESIRPALELSKASVTKCSISKLELSAQBELLTTPSLESLVSGTIOGDOIFPN--L 1098  
 DB 858 agsislvlstck-nlyslwaeasplteclerhltstnltklsih---dlqgrtppgl 913  
 OY 1099 DKFLCLKELSVDLGCINVFVPIPEEPNFMHEKLLIOISAEPYSKYKLIOMSPMLH 1158  
 DB 914 dsignlknltklmldnklm-----needaiklaegllknklkmc 951  
 OY 1159 VFHLKCNFESDFGSLMTMLVS-----CKKLKIFSDSFF--QAVPVA-SLPNFTSLK 1209  
 DB 952 lfhl--thlsldgmgndylvklslsepc-dleelqivscclsaavkllaqnlhnlvks 1008  
 OY 1210 IINLEGOQPPDETSKFAVILGSLNLEE--LILPGDGYRAKLIQOQCOQLNCLR 1266  
 DB 1009 lldl--senylekdgneahellidrmvleqltalmlpgcdvgsjsllkhlvevqylv 1067  
 OY 1267 VLSFKTLMDSDVVEIAKVAISGCF-----QKLENKLSLNHKTTEGYRNFQALDNM 1320  
 DB 1068 klgikmwlrtcd-----eirlgafgknpklngqinlagn--vssadgyvafmgvfenl 1121  
 OY 1321 PVLQELDISRHFTCEIKQAQVTVKSLSCQVLRPLRLNLNLSVLDDADIALNLNWKER 1380  
 DB 1122 kqlvffdfs--ctkeflpdpalvrlkqlsvlsklftfgearlvgwgfoddlsvldekeq 1178  
 OY 1381 HPOSXYTLTILOKMLPSP 1399  
 DB 1179 -----mlcpwvixkllp 1189

RESULT 10







Db 877 vlegltalmipwcdvgsissllkhlvevpqvlkglknwrltdt-----elrllgaff 931  
QY 1292 -----QKLENKLSTINHKITEGYNRFQALDMPNLOELDISRHFTETICKAQTIVKSL 1346  
Db 932 gknpjknfgqjnlagn-rvssdgwlaimgvfenlkqjlvfdts---tkeflpdpalvrl 987  
QY 1347 SOCVLRPLRLRLNMLSMILLDADIAL 1374  
Db 988 sqvisklftlgearlvwgqfdddlsvl 1015

RESULT 12  
AAM23595  
ID AAM23595 standard; Protein; 841 AA.  
AC AAM23595;  
DT 12-OCT-2001 (first entry)  
DE Murine EST encoded protein SEQ ID NO: 1120.  
XX  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
XX diagnostics; forensic test; gene mapping; genetic disorder;  
XX biodiversity; gene therapy; nutrition.  
OS Mus musculus.  
XX  
XX WO200154477-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-US02687.  
XX  
XX 25-JAN-2000; 2000US-0491404.  
XX PR 17-JUL-2000; 2000US-0617746.  
XX PR 03-AUG-2000; 2000US-0631451.  
XX PR 15-SEP-2000; 2000US-0663870.  
XX  
XX (HWE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
XX Cao Y, Dermanac RA, Zhang J, Werhman T;  
XX  
XX WPI: 2001-476164/51.  
XX DR N-PSDB; AAH98254.  
XX  
XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
XX antibodies and research use -  
XX  
XX Claim 20; Page 832-833; 1275pp; English.  
XX  
XX The present invention provides the protein and coding sequences of novel  
XX proteins from a variety of organisms, including human, dog, cat, horse,  
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)  
XX from the organism of interest. They can be used in diagnostics,  
XX forensics, gene mapping, identification of mutations, to assess  
XX biodiversity and for nutritional purposes. The present sequence is a  
XX protein of the invention.  
XX  
XX Sequence 841 AA;  
XX

Query Match 7.7%; Score 566; DB 22; Length 841;  
Best Local Similarity 23.5%; Pred. No. 3, 1e-38;  
Matches 226; Conservative 174; Mismatches 359; Indels 202; Gaps 36;

QY 486 LWASGCCPLLNRLVLYSLSTRPDEGLASTICDQLLEKESVTEKMRNITQOLKNO 545  
Db 2 lvgsgkckalktkfivfifrlis--raggllfclcdqllidiprltkqtfmamlklrqr 59  
QY 546 VLFLDDYKICSIPO---VIGKLIQKNLSTRCLLIAVRTNARDIRRYLFTLEIKAF 602

Db 60 vlflldgynef--kpnqnceieallkenhrfkmmvltvtteclrlirfgalteevgm 117  
QY 603 PEYNTVCILRKLESHNMTRLRKRMVYFGKNOSLOKIQKTPLEVAIAICAHFOYPDPSD 662  
Db 118 tedsaqallrevllikela--eglllqgksrcrlnmktplfvltlcalqmgsefshnt 175  
QY 663 DVAVFYSYMERLSLRK-----ATRAELIKATVSSGGLALGFPSCCFEFDNDLAEAG 716  
Db 176 qtlfhtlydillqknkhkhkgyaaadflr-sldhgyalalegvishktdfelqdv--ss 232  
QY 717 VDEEDLTWCLMSKFPQAQRPFYRFLSPAQEFLAGMLRLLELDDROEHODIGLYHKK 776  
Db 233 vnedvlltclgllckytaqfkkpkkfthksfgyetagrllsslltshpeevtkngylyq 292  
QY 777 QINSPMTVSAYNNFLNVY--SSLPTKAGPKIVSHLLHVDN-----KE 819  
Db 293 kmvslsdlstysllrycgssveatra---vmkhlaevyqhgcllgistakrplwrqe 349  
QY 820 SLENISENDYLKHQPEISLOMOLRGLMOICQAVFSMVSEHLLVLAKTAVQST-VA 878  
Db 350 slqsvkn-----tlegellkal---nlhsfvecgllh-----ygestsk 386  
QY 879 ACSPEVLOPLOGRTLTGALNL-QYFDPHPESTLSLSIHFPTRGKNTSPRAHFSVLETC 937  
Db 387 alsqefaeffgqkslyinsgnlpdyldfde-----hlp-----420  
QY 938 FDKSQVPTIDQYASAFE-----PMEWERNLAEKEDNVKSYMOMORRASPDLSTG 988  
Db 421 -----ncasaldflklgygamasve-----Kaedtgyl 451  
QY 989 YKLSPKOYKIP-----CLEVDNDIDVYGOMLELMTVFASQRIELH 1033  
Db 452 hmeepely-tpstravslfnwqgeftrlevlrdtsklnkqdlrlygkifsaatslrq 510  
QY 1034 LNHSGFISIRPALBELSKASVTKCSISKLELSAABQELLTPSLESLEVSQTIQSDQ 1093  
Db 511 krcagvagslsavlstck-nlyslmveaspltdederhltsvtnlktlsih--dlqng 566  
QY 1094 IFPN--LDKFLCLKELSVDLEGNINVSVPPEFPNHHMKLLIOISAEYPSKLVKLI 1151  
Db 567 rlpjgltldslgnlknltklimdnkm-----needaiklaeg1 604  
QY 1152 QNSPNLHVHFLKCNFSDSGSLMTMLVS-----CKKLEIKSDSF--QAVPFA-SL 1202  
Db 605 knlkmclthl--thlsdligmdyivkslsepc-dleelqivscslsanaakllagnl 661  
QY 1203 PNFIISLIINLEGOQPPDEETSEKFAVITLSLSNLEE---LILPTGDIYRAKLITQOC 1259  
Db 662 hnlvkslidl-senylekdgnealhelldrmvleqlcalmipwcdvgsissllkhl 720  
QY 1260 QQLHCLRVLSFEKTLNDSDVYEIAKVAISGCF-----QKLENKLSTINHKITEBYRNF 1313  
Db 721 eevpqvlkglknwrltdt-----elrllgaffgknplknfgqjnlagn-rvssdgwla 774  
QY 1314 FOALDMPNLOELDISRHFTETICKAQTIVKSLSOVLRPLRLRLNMLSMILLDADIAL 1373  
Db 775 mgyfenlkqjlvfdts---tkeflpdpalvrlsqvisklftlgearlvwgqfdddlsv 831  
QY 1374 L 1374  
Db 832 I 832

RESULT 13  
AAB53493  
ID AAB53493 standard; Protein; 118 AA.  
XX AAB53493;  
XX  
XX 09-MAR-2001 (first entry)  
XX  
XX Human colon cancer antigen protein sequence SEQ ID NO:1033.  
XX

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW Identification: cytostatic; cardioactive; neuroprotective; vulnerary;  
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;  
 KW nephrotoxic; antineoplastic; antibacterial; gene therapy; wound;  
 KW neutral disorder; immune system disorder; muscular disorder;  
 KW reproductive disorder; gastroenterological disorder; renal disorder;  
 KW infectious disease; cardiovascular disorder;  
 OS Homo sapiens.  
 PN WO200053531-A1.  
 PD 21-SEP-2000.  
 PF 08-MAR-2000; 2000WO-US05883.  
 PR 12-MAR-1999; 99US-0124270.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Ruben SM;  
 DR WPI: 2000-587534/55.  
 DR N-PSDB: AAC98250.  
 PT Colon cancer associated gene sequences, referred to as colon cancer  
 PT antigens, useful for the treatment, prevention, and diagnosis of colon  
 XX disorders such as colon cancer -  
 XX  
 XX Claim 11: Page 1612; 2104pp; English.  
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,  
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The  
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;  
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,  
 CC vulnerary, nephrotoxic, antineoplastic, antibacterial, gene therapy, wound,  
 CC neutral disorder, immune system disorder, muscular disorder, and  
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,  
 CC proteins and antibodies to the proteins are useful for the prevention,  
 CC treatment and diagnosis of colon disorders, such as colon cancer. The  
 CC polynucleotides may be used in diagnostics and research, such as for  
 CC chromosome identification, and as hybridisation probes. The proteins  
 CC may also be used to prevent diseases such as neural disorders, immune  
 CC system disorders, muscular disorders, reproductive disorders, immune  
 CC gastrointestinal disorders, wounds, renal disorders, infectious  
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and  
 CC AAB54007 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 118 AA:  
 SQ  
 Query Match  
 Best Local Similarity 7.5%; Score 545.5; DB 21: Length 118;  
 Matches 106; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
 Oy 607 TVCILRLKLFSHNTRLRKFFVYFGKNSLOKOTPLFAAICAHWPYPPDPSPDVAV 666  
 Db 1 TVCILRLKLFSHNTRLRKFFVYFGKNSLOKOTPLFAAICAHWPYPPDPSPDVAV 666  
 Oy 667 FKSYMERLSLRNKATAEILKATVSSCGELALKGFSCCFEEND-DDLAEG 716  
 Db 61 FKSYMERLSLRNKATAEILKATVSSCGELALKGFSCCFEEND-DDLAEG 716  
 RESULT 14  
 ID AAC67526 standard; Protein: 738 AA.  
 AC AAC67526;  
 XX  
 XX 26-NOV-2001 (first entry)  
 DT  
 XX

DE Amino acid sequence of a human secreted polypeptide.  
 XX  
 KW Human; secreted polypeptide; nervous disease; muscular disease; tumour;  
 KW gastrointestinal ulceration; spinal cord disease; trachea disease;  
 KW thyroid gland disease; ovary disease; prostate disease; heart disease;  
 KW renal gland disease; small intestine disease; thymus disease;  
 KW lymph node disease; muscular system disease; colon disease;  
 KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;  
 KW myocardial infarction; angioplasty; liver disease; coagulation disorder;  
 KW microbial disease; immune disorder; inflammation; transplant rejection;  
 KW bone thickness; bone density; ferroxidase loss; apoptosis;  
 XX  
 XX  
 XX  
 OS Homo sapiens.  
 PN WO200166690-A2.  
 PD 13-SEP-2001.  
 PF 05-MAR-2001; 2001WO-US07143.  
 PR 06-MAR-2000; 2000US-0187107.  
 PR 13-MAR-2000; 2000US-0188916.  
 PR 03-OCT-2000; 2000US-0236874.  
 PR 03-OCT-2000; 2000US-0237846.  
 PA (SMK ) SMITHKLINE BEECHAM CORP.  
 PA (SMK ) SMITHKLINE BEECHAM PLC.  
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 DR WPI: 2001-570768/64.  
 DR N-PSDB: AAB78218.  
 XX  
 XX  
 XX Novel isolated secreted polypeptide useful for treating nervous and  
 PT muscular diseases, gastrointestinal ulceration, coagulation and immune  
 PT disorders, microbial diseases, inflammation and transplant rejection -  
 XX  
 XX  
 XX Claim 1: Page 89-91; 102pp; English.  
 CC  
 CC The present sequence represents a human secreted polypeptide. The  
 CC secreted polypeptides and polynucleotides are useful for treating  
 CC nervous and muscular diseases, for inhibiting tumour formation and  
 CC metastasis, for treating gastrointestinal ulceration, for preventing  
 CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
 CC renal gland, small intestine, heart, trachea, thymus, lymph node,  
 CC muscular system and colon, for treating lipase deficiency in cystic  
 CC fibrosis and pancreatitis, for treating undesirable clot formation in cystic  
 CC such as myocardial infarction, during angioplasty and all surgical  
 CC procedures that require decreased blood clot formation, for treating  
 CC liver diseases, coagulation disorders and microbial diseases, for  
 CC treating immune disorders, for treating inflammation and transplant  
 CC rejection, for enhancing bone thickness and increasing bone density,  
 CC apoptosis, and for regulating vascular smooth cell proliferation. They  
 CC may also be used as vaccines.  
 XX  
 XX  
 XX Sequence 738 AA:  
 SQ  
 Query Match  
 Best Local Similarity 7.3%; Score 536.5; DB 22: Length 738;  
 Matches 197; Conservative 142; Mismatches 285; Indels 181; Gaps 29;  
 Oy 344 FLONMKS-SAEVTPDQSRLELLETSSNLEDSIAVGPVPEMAGGEQWQEKKN 402  
 Db 55 FLKIKEMYPILFGDINGQ-----SLFHTSGEGDLD----- 86  
 Oy 403 LNEQURAAYTSASFRRHMSLDISSDLATDHLGCDLST---ASKHISKPV----- 449  
 Db 87 LAGDILKDIYHCPISFLNF-----YPIGEDIDILFNLKSLFTEPVYLRKQDQHHR 134  
 Oy 450 QEPVLVLPVEVFGNLSVMCVGEAGSGKTVLLKIAFLMASGCCPLNLRNPOLYVFLSLST 509

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Db      135 veqtlngllqalspcilegesgkgtcllqrlamlwsgskckalstkfkfvtffrls-- 192
Qy      510 RPDGLASITCDLLEKSGSTEMCMRNIIOQLKNQVFLDDKREISIQ--VIGKL 566
Db      193 raqgglfctclcdqldlpgtlrktcfmamlklqrvflldgynef--kqncpeal 250
Qy      567 IOKNHLSTCLLIIVRTARRADIRRELTLEIKAFPFYNVCIRKLFSHNMFTLRKFM 626
Db      251 lkenhrfmmvlttctecclhltqfgaltaevgmtedsaqalirevllkela--egll 308
Qy      627 VYFGKNSIQRIOKTPLEVAACAHMFQYPPDPSPDVAVERKSYMERLSLRNK-----A 680
Db      309 lqldqsrclrlmkrplvtlcalqmgesehfshltqtlftftfydlilqmkhkhkgya 368
Qy      681 TAEIIKATVSSCGELATGKGFSCCFEENDDLAEGVDEDELTMCILMSKPTAQLRPFY 740
Db      369 asdftr-sldhcgdlalegvfshktdfaldgv--ssvnedvlltqgllckytaqrfkpk 425
Qy      741 RFLSPAFQEFILAGMRLEILDSDRQEHODLGLYHLKQINSPMMVTSAVNNFLNYY--SSL 798
Db      426 kfhkstfeytaqrrllslltshepevltkngyldkmvslsdltscysallrytcgssv 485
Qy      799 PSTKAGPTIVSHLHLVNN-----KESLENISENDYLUKHQPEISIQMQL 843
Db      486 eatra---vmkhlaavyghgcllgtsiakrplrqeslqsvkn-----tlegel 531
Qy      844 LRGLMQIQPQAFVSMVSHLVLVLAKTAYQSNF--VAACSPVYLOLQGRITLGLALN--Q 901
Db      532 lka1---nlnstfvecgihl-----ygestskalsqefeafigklslyinsgnl 579
Qy      902 YFFDHPESLILRSIHPIRGNKTSRAHFSVLETCFDSQVPTIDDOYASAFEDPMME 961
Db      580 ylfid-----fnehlpnc--asaifkldifyg--amaawe 611
Qy      962 RNLAEKEDNVKSYMQRASPDLSTGYWKLSPKQYKIP-----CLEVDY 1006
Db      612 -----kaeedtgylmeepely-lpsravslffmwkgqfrelvtl 652
Qy      1007 NDIDVVGDMLEILMTVVSASGRIRLHLNHSNGFTESIRPALELSKASVTKCSIKLEIS 1066
Db      653 rdfsrlnkqdlrlylqkllssatsrlqlkrcagvagslsvlstock-nlyslmveaspl 711
Qy      1067 AAEOELLTLPLESLSEVSGTOSQ 1091
Db      712 ldeerhltsvtnlklcslin-dlqng 735

RESULT 15
AAW19746
ID      AAW19746 standard; Protein: 618 AA.
AC      AAW19746;
XX      16-SEP-1997 (first entry)
DE      Human inhibitor of apoptosis protein homologue MIH8.
XX      Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIH8;
KW      degenerative disease; infectious disease; autoimmune disease;
RW      cancer; therapy; diagnosis.
XX      Homo sapiens.
XX      OS
XX      FH      Location/Qualifiers
XX      FT      46..113
XX      FT      /label= BIR
XX      FT      184..250
XX      FT      /label= BIR
XX      FT      269..337
XX      FT      /label= BIR
XX      FT      569..606
XX      FT      /label= RING_finger

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XX      009723501-A1.
PN      03-JUL-1997.
PD      20-DEC-1996; 96WO-AU00827.
PF      22-DEC-1995; 95AU-0007275.
PR      (AMRA-) AMRAD OPERATIONS PTY LTD.
PA      Vaux DL;
PI      WPI: 1997-350966/32.
DR      N-PSDB: AAT72711.
XX      Isolated protein homologues of viral inhibitors of apoptosis - used
PT      to modulate apoptosis for treatment of degenerative, infectious or
PT      autoimmune diseases and cancer
XX      Claim 8; Page 51-54; 136pp: English.
PS      Mammalian IAP homologue B (MIH8) (AAW19746) is a human homologue of
CC      baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC      sequence was deduced from a cDNA clone (see also AAT72711) isolated
CC      from a human foetal liver cDNA library using primers based on
CC      human EST sequences that resembled the BIR repeats of Orygia
CC      pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also
CC      AAW19745 and AAW19747-52) and their derivatives and chemical analogues
CC      can be used in methods for modulating apoptosis in animal cells,
CC      specifically for treatment, by inhibition, of degenerative and
CC      infectious disease or, by promotion, of cancer and autoimmune
CC      disease.
XX      Sequence 618 AA:
SQ

Query Match      6.3%; Score 462; DB 18; Length 618;
Best Local Similarity 26.0%; Pred. No. 1,1e-29;
Matches 155; Conservative 82; Mismatches 218; Indels 146; Gaps 22;

Qy      38 LEEEDOKERAKMKQKQNSQMRSEARKLRTFYVEPYSSWIP---QEMAAAGFYTVKSG 94
Db      28 lsdwensnkqkmkydfsee-----lymstyslfpqypvsetslraglylgvndk 80
Qy      95 IQFCFCSLILFAGLRLPIEDHKRFRHPDCGF---LKKDGNIAKYDIRVKN----- 144
Db      81 vkfcfcgimldmwlkigdspiqkqlypscfiqlnlvaslqstsktsktspmnsfahals 140
Qy      145 -----LKSRL-----RGKMKRY--QEEFARLASFRNNPFYVG 175
Db      141 ptlehsalffsgysalspnplnsraveldssrtltpysamsteaarlilylmwp--llf 198
Qy      176 ISPCVISEAGFYFTGKODTVOCFSCGCGCLGNNEEGDPMWEKAKWPKCEFRKSSSEE 235
Db      199 lspselaragflyigpdtvacfaagylsmwepkddamsehrfipncplf---ensle 255
Qy      236 ITQYIQSYKGFVDITGEHFVNSWQRELPMASAYCNDSTIFAEELRLDSFKDMPRESAVG 295
Db      256 tlrfsls-----nlsmqt-----haartmrlfmywpsvpyq 286
Qy      296 VAALAKAGLFYTGINDIVOCFSCGCLGKMWGCDPDLDDHTRCFPNCPLQNMKSSAEVT 355
Db      287 peglasagflyvgrndvkcctcdgdlctwesgdppwehakiwlrpceflilmkqg-efv 345
Qy      356 PDQGR-GEIACEILETTSESNNLEDSIAVGPIPEMAOGCEAOWFOEAKMLNEQLRAAYTSA 414
Db      346 delgrryphllleqllstsdtegen--adpplihgpgess--sedavmmntprvvsaleem 402
Qy      415 SFRHMSLDDISSDLATDHLILGCDLSIAKHKISKPVQEP--LVLPVFGNLNYSVMEYGEAG 473
Db      403 gfnr-----dl-----vkvtvsgsklltltgenyktvndivsalinae 438

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OY 474 SGTVLK-KIAFLMNSGCCPLNRFOLVFLSLSTRPDEGLASICDQLEKEGSYTE 532  
Db 439 dekreeekqaeasddlsllrkrmalfqglecvlp-----lIdnllk----- 484  
OY 533 MCMRNIOQLKNOVLFLLDYKEICISIPOVIGKIQKNHLSRTCLLZAVRTNRARDI 589  
Db 485 ---anvlnkqehdl-----kqktqplqarelId-----tlvkgnaaanl 523

Search completed: September 30, 2002, 15:04:43  
Job time: 324 sec

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OM protein - protein search, using sw model

Run on: September 30, 2002, 15:00:54 : Search time 19.98 Seconds  
(without alignments)  
1715.171 Million cell updates/sec

Title: US-09-830-338-1  
Perfect score: 7308  
Sequence: 1 MATOQKASDERISQFDHNL.....SKYTLILQKWLPSPILQK 1403

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCUOS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	6373.5	87.2	1232	US-08-836-134-2	Sequence 2, Appli
2	5955	81.5	1151	US-08-836-134-23	Sequence 23, Appli
3	462	6.3	618	US-08-511-485-8	Sequence 8, Appli
4	462	6.3	618	US-09-212-971-8	Sequence 8, Appli
5	462	6.3	618	US-08-800-929A-8	Sequence 8, Appli
6	462	6.3	618	US-08-569-749-2	Sequence 2, Appli
7	462	6.3	618	US-09-617-053A-8	Sequence 8, Appli
8	462	6.3	618	US-09-069-023-29	Sequence 29, Appli
9	462	6.3	618	PCT-US96-12860-2	Sequence 2, Appli
10	457.5	6.3	612	US-09-212-971-14	Sequence 14, Appli
11	457.5	6.3	612	US-08-800-929A-14	Sequence 14, Appli
12	457.5	6.3	612	US-08-569-749-14	Sequence 14, Appli
13	457.5	6.3	612	US-09-617-053A-14	Sequence 14, Appli
14	457.5	6.3	612	PCT-US96-12860-14	Sequence 14, Appli
15	440	6.0	600	US-09-212-971-12	Sequence 12, Appli
16	440	6.0	600	US-08-800-929A-10	Sequence 10, Appli
17	440	6.0	600	US-09-617-053A-12	Sequence 12, Appli
18	437.5	6.0	496	US-08-511-485-10	Sequence 10, Appli
19	437.5	6.0	496	US-09-212-971-10	Sequence 10, Appli
20	437.5	6.0	496	US-08-800-929A-10	Sequence 10, Appli
21	437.5	6.0	496	US-09-617-053A-10	Sequence 10, Appli
22	436.5	6.0	604	US-08-569-749-4	Sequence 4, Appli
23	436.5	6.0	604	PCT-US96-12860-4	Sequence 4, Appli
24	431.5	5.9	604	US-08-511-485-6	Sequence 6, Appli
25	431.5	5.9	604	US-09-212-971-6	Sequence 6, Appli
26	431.5	5.9	604	US-08-800-929A-6	Sequence 6, Appli
27	431.5	5.9	604	US-09-617-053A-6	Sequence 6, Appli

28	403	5.5	497	2	US-08-511-485-4	Sequence 4, Appli
29	403	5.5	497	3	US-09-212-971-4	Sequence 4, Appli
30	403	5.5	497	4	US-08-800-929A-4	Sequence 4, Appli
31	403	5.5	497	4	US-09-617-053A-4	Sequence 4, Appli
32	340.5	4.7	438	5	PCT-US95-05922A-2	Sequence 2, Appli
33	337	4.6	498	2	US-08-511-485-13	Sequence 13, Appli
34	303.5	4.2	275	2	US-08-511-485-12	Sequence 12, Appli
35	303.5	4.2	275	3	US-08-836-134-21	Sequence 21, Appli
36	293.5	4.0	268	3	US-08-836-134-22	Sequence 22, Appli
37	290	4.0	50	4	US-08-975-080-26	Sequence 26, Appli
38	261	3.6	47	4	US-08-975-080-13	Sequence 13, Appli
39	212.5	2.9	68	2	US-08-511-485-27	Sequence 27, Appli
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42	207.5	2.8	68	2	US-08-511-485-26	Sequence 26, Appli
43	200.5	2.7	68	2	US-08-511-485-20	Sequence 20, Appli
44	196.5	2.7	68	2	US-08-511-485-21	Sequence 21, Appli
45	185.5	2.5	68	2	US-08-511-485-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1  
US-08-836-134-2  
; Sequence 2, Application US/08836134A  
; Patent No. 6020127  
; GENERAL INFORMATION:  
; APPLICANT: Mackenzie, Alex E.  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mahadevan, Mani S.  
; APPLICANT: Mclean, Michael  
; APPLICANT: Roy, Natalie  
; APPLICANT: Ikeda, John  
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and  
; Patent No. 6020127  
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy  
; FILE REFERENCE: 3477-112, 033477/139914  
; CURRENT APPLICATION NUMBER: US/08/836,134A  
; CURRENT FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-08-836-134-2

Query Match 87.2% Score 6373.5; DB 3; Length 1232;  
Best Local Similarity 95.9% Pred. No. 0;  
Matches 1229; Conservative 1; Mismatches 1; Indels 51; Gaps 1;

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DB	1	MATQKASDERISQFDHNLPELSALLGLDAVOLAKLEEEBOKERAKKQKNSQMRSE	60
QY	61	AKRLTFVYEPYSSNIPDEMAAGFYFVGVSIGIOCFCCSILIFGAGLTRLPIDHKRF	120
DB	61	AKRLTFVYEPYSSNIPDEMAAGFYFVGVSIGIOCFCCSILIFGAGLTRLPIDHKRF	120
QY	121	HPDCGLLNKDVGNIAKYIRVKNLSRLRGKMRQEEEARLASFRNMPFYVGISPCV	180
DB	121	HPDCGLLNKDVGNIAKYIRVKNLSRLRGKMRQEEEARLASFRNMPFYVGISPCV	180
QY	181	LSEAGFVFTGKODVOCFSCGCLGNMBEGDDPWKEHAKWPKCFELRSKSSSEITQYI	240
DB	181	LSEAGFVFTGKODVOCFSCGCLGNMBEGDDPWKEHAKWPKCFELRSKSSSEITQYI	240
QY	241	OSYKGFVDITGHEFVNSVQRELPMASAYCNDISIFAYEELRLDSFKWPRESAVGYAALA	300
DB	241	OSYKGFVDITGHEFVNSVQRELPMASAYCNDISIFAYEELRLDSFKWPRESAVGYAALA	300

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DB 301 KAGLEFYTGKIDIVOCFCGCGGLEKMOEGDPLDDHTRCFPNCPFLONKSSAEVTPDIQS 360  
QY 361 RGEICELLETTSESNNLEDSIAVGP IYVEMAGCEAQMFOEAKNLNOLRAATTSASFRRMS 420  
DB 361 RGEICELLETTSESNNLEDSIAVGP IYVEMAGCEAQMFOEAKNLNOLRAATTSASFRRMS 420  
QY 421 LLDISSDLATDHLGCDLSIAASKHISKPYOEPLVPEVFGNLNSVCKVEGASGKTIVLL 480  
DB 421 LLDISSDLATDHLGCDLSIAASKHISKPYOEPLVPEVFGNLNSVCKVEGASGKTIVLL 480  
QY 481 KKIAPLMASSCCPLNLRPOLVFLYLSSTRPDEGLASTICQOLLEKGSYTEKMCNRIIO 540  
DB 481 KKIAPLMASSCCPLNLRPOLVFLYLSSTRPDEGLASTICQOLLEKGSYTEKMCNRIIO 540  
QY 541 QLNQOVFLDDYKEIGSIPOVIGKLTOKNHLSTRTCLLAVRTNRARDIRRYLETILEIQ 600  
DB 541 QLNQOVFLDDYKEIGSIPOVIGKLTOKNHLSTRTCLLAVRTNRARDIRRYLETILEIQ 600  
QY 601 APFPYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOK IOKTLPVAAICAHMFQYPPDPS 660  
DB 601 APFPYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOK IOKTLPVAAICAHMFQYPPDPS 660  
QY 661 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFERNDDDLAAGVDED 720  
DB 661 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFERNDDDLAAGVDED 720  
QY 721 EDLTMLCKSFTNQRRLRPYRFLSPAFQEFLAGMRLLIELDSDBOEQODIGLYHLKQINS 780  
DB 721 EDLTMLCKSFTNQRRLRPYRFLSPAFQEFLAGMRLLIELDSDBOEQODIGLYHLKQINS 780  
QY 781 PMHTVSAVNNFLNVYSSLPTFKAGPKIVSHLLHLVDNKESELENISENDYDLKHOPEISIQ 840  
DB 781 PMHTVSAVNNFLNVYSSLPTFKAGPKIVSHLLHLVDNKESELENISENDYDLKHOPEISIQ 840  
QY 841 MOLLNGLMOICPOAVFESVSEHLVYALKTAYOSNTVAACSPRYLOFQGRITLIGALNT 900  
DB 841 MOLLNGLMOICPOAVFESVSEHLVYALKTAYOSNTVAACSPRYLOFQGRITLIGALNT 900  
QY 901 QYFDPHPSLSLRSHIRPGNKTSPPRAHFVLETCGPKSGVPTIIDODVSAFEPNEN 960  
DB 901 QYFDPHPSLSLRSHIRPGNKTSPPRAHFVLETCGPKSGVPTIIDODVSAFEPNEN 960  
QY 961 ERNLAEKEDVNSKYMOMORASPDLSGTGYKLSPKOYKIPCLEVDVNDIDVQODMLETL 1020  
DB 961 ERNLAEKEDVNSKYMOMORASPDLSGTGYKLSPKOYKIPCLEVDVNDIDVQODMLETL 1020  
QY 1021 MTFVSAOSRIELHNSRGFIIESIRPALELSKASVTKCSISKLELSAAEOELLTLPSLE 1080  
DB 1021 MTFVSAOSRIELHNSRGFIIESIRPALELSKASVTKCSISKLELSAAEOELLTLPSLE 1080  
QY 1081 SLEVSGTTIOSODQIFPNLDKFLCKELSYDLBGNINVFVSIPEEPFNHMEKLLIOISA 1140  
DB 1081 SLEVSGTTIOSODQIFPNLDKFLCKELSYDLBGNINVFVSIPEEPFNHMEKLLIOISA 1140  
QY 1141 EYDSKLVKLIONSPNLHVHLKCNFSDRGLMTMLVSCKKTLEIKRSDSFPQAVPRVA 1200  
DB 1141 EYDSKLVKLIONSPNLHVHLKCNFSDRGLMTMLVSCKKTLEIKRSDSFPQAVPRVA 1200  
QY 1201 SLPRFTSLKLTLEGOQFPODEETSEKFAVITIGLSNLEELLTPRGDGIYRAKLLIOQCO 1260  
DB 1201 SLPRFTSLKLTLEGOQFPODEETSEKFAVITIGLSNLEELLTPRGDGIYRAKLLIOQCO 1260  
QY 1261 QLNHCLRVLSFFFTLNDSDVVEI 1282  
DB 1261 QLNHCLRVLSFFFTLNDSDVVEI 1282  
QY 1210 QLNHCLRVLSFFFTLNDSDVVEI 1231  
DB 1210 QLNHCLRVLSFFFTLNDSDVVEI 1231

RESULT 2  
US-08-836-134-23  
; Sequence 23, Application US/08836134A  
; Patent No. 6020127

GENERAL INFORMATION:  
APPLICANT: Mackenzie, Alex E.  
APPLICANT: Kornejuk, Robert G.  
APPLICANT: Mahadevan, Mani S.  
APPLICANT: McLean, Michael  
APPLICANT: Roy, Natalie  
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and  
Patent No. 6020127  
FILE REFERENCE: Mutations Causing of Spinal Muscular Atrophy  
CURRENT APPLICATION NUMBER: US/08/836,134A  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 23  
LENGTH: 1151  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-836-134-23

## Query Match

Best Local Similarity 81.5%; Score 5955; DB 3; Length 1151;  
Matches 1139; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATQOASASERTSOFDHNLLPELSALGLDAVOLAKLEEEDEKERRAKMOGYNSQMRSE 60  
DB 10 MATQOASASERTSOFDHNLLPELSALGLDAVOLAKLEEEDEKERRAKMOGYNSQMRSE 60  
QY 61 ARKLFTVYERYESSWIPQEMAAAGFTGVKSGIQFCCSILFLFGAGLTRPIDHNR 120  
DB 70 ARKLFTVYERYESSWIPQEMAAAGFTGVKSGIQFCCSILFLFGAGLTRPIDHNR 120  
QY 121 HPDCGFLNKNVGNINATYDRVAKLSRLRGKMRQOEERLASFRRMPPYVQGISPCV 180  
DB 130 HPDCGFLNKNVGNINATYDRVAKLSRLRGKMRQOEERLASFRRMPPYVQGISPCV 180  
QY 181 LSENGFVTGKODTVOCFSCGCGLEKMOEGDPLDDHTRCFPNCPFLONKSSAEVTPDIQS 360  
DB 190 LSENGFVTGKODTVOCFSCGCGLEKMOEGDPLDDHTRCFPNCPFLONKSSAEVTPDIQS 360  
QY 241 QSYKGFVDITGEHFVNSVQRELPMASAYCNDISIFAYEBELRDSFDMRESAVGAALA 300  
DB 250 QSYKGFVDITGEHFVNSVQRELPMASAYCNDISIFAYEBELRDSFDMRESAVGAALA 300  
QY 301 KAGLEFYTGKIDIVOCFCGCGGLEKMOEGDPLDDHTRCFPNCPFLONKSSAEVTPDIQS 360  
DB 310 KAGLEFYTGKIDIVOCFCGCGGLEKMOEGDPLDDHTRCFPNCPFLONKSSAEVTPDIQS 360  
QY 361 RGEICELLETTSESNNLEDSIAVGP IYVEMAGCEAQMFOEAKNLNOLRAATTSASFRRMS 420  
DB 370 RGEICELLETTSESNNLEDSIAVGP IYVEMAGCEAQMFOEAKNLNOLRAATTSASFRRMS 420  
QY 421 LLDISSDLATDHLGCDLSIAASKHISKPYOEPLVPEVFGNLNSVCKVEGASGKTIVLL 480  
DB 430 LLDISSDLATDHLGCDLSIAASKHISKPYOEPLVPEVFGNLNSVCKVEGASGKTIVLL 480  
QY 481 KKIAPLMASSCCPLNLRPOLVFLYLSSTRPDEGLASTICQOLLEKGSYTEKMCNRIIO 540  
DB 490 KKIAPLMASSCCPLNLRPOLVFLYLSSTRPDEGLASTICQOLLEKGSYTEKMCNRIIO 540  
QY 541 QLNQOVFLDDYKEIGSIPOVIGKLTOKNHLSTRTCLLAVRTNRARDIRRYLETILEIQ 600  
DB 550 QLNQOVFLDDYKEIGSIPOVIGKLTOKNHLSTRTCLLAVRTNRARDIRRYLETILEIQ 600  
QY 601 APFPYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOK IOKTLPVAAICAHMFQYPPDPS 660  
DB 610 APFPYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOK IOKTLPVAAICAHMFQYPPDPS 660  
QY 661 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFERNDDDLAAGVDED 720  
DB 670 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFERNDDDLAAGVDED 720

QY	721	EDLMCLMSKFTAO	RLBPFRPLSPAPQELGMRLEILLDSRQEHODGLYHLKQINS	780
Db	730	EDLMCLMSKFTAO	RLBPFRPLSPAPQELGMRLEILLDSRQEHODGLYHLKQINS	789
QY	781	PMATVSAYNNFL	NAVSSLPSTKAGPKIVSHLLHLVDNKESELENISENDYLKHQPEISLQ	840
Db	790	PMATVSAYNNFL	NAVSSLPSTKAGPKIVSHLLHLVDNKESELENISENDYLKHQPEISLQ	849
QY	841	MOLLRLGLMOIC	POAYFBSMVBSEHLVLALKTATQNSNTVAACSPFYLOFLOGRTLYLGALNL	900
Db	850	MOLLRLGLMOIC	POAYFBSMVBSEHLVLALKTATQNSNTVAACSPFYLOFLOGRTLYLGALNL	909
QY	901	QYFEDHESLSLR	SIFRPFRGNKTSPPRAHFSVLETCFPRKSQVPTIDODYASAFEPNEM	960
Db	910	QYFEDHESLSLR	SIFRPFRGNKTSPPRAHFSVLETCFPRKSQVPTIDODYASAFEPNEM	969
QY	961	ERNIAEKEDNVK	SYMOMORRASPDLSTGYWKLSPKOYKIRPCELVVDNIDVVGQDMETL	1020
Db	970	ERNIAEKEDNVK	SYMOMORRASPDLSTGYWKLSPKOYKIRPCELVVDNIDVVGQDMETL	1029
QY	1021	MTVSAASORIE	LHNHNRGTIESIRPALELSASAYTKGCSISLELSAAEQELLTLTPELE	1080
Db	1030	MTVSAASORIE	LHNHNRGTIESIRPALELSASAYTKGCSISLELSAAEQELLTLTPELE	1089
QY	1081	SLEVSGETIGSOD	OIFPMLDLFLCLLKLSTVDLGNINIVFVIREEPFNNHHEKLLIQISA	1140
Db	1090	SLEVSGETIGSOD	OIFPMLDLFLCLLKLSTVDLGNINIVFVIREEPFNNHHEKLLIQISA	1149
QY	1141	E	1141	
Db	1150	E	1150	

RESULT 3  
 US-08-511-485-8  
 \* Sequence 8, Application US/08511485  
 \* Patent No. 5919912  
 \* GENERAL INFORMATION:  
 \* APPLICANT: Korneljuk, Robert G.  
 \* APPLICANT: Mackenzie, Alexander E.  
 \* APPLICANT: Baird, Stephen  
 \* TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS  
 \* TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
 \* NUMBER OF SEQUENCES: 38  
 \* CORRESPONDENCE ADDRESS:  
 \* ADDRESSEE: Fish & Richardson P.C.  
 \* STREET: 225 Franklin Street  
 \* CITY: Boston  
 \* STATE: MA  
 \* COUNTRY: USA  
 \* ZIP: 02110-2804  
 \* COMPUTER READABLE FORM:  
 \* MEDIUM TYPE: Floppy disk  
 \* COMPUTER: IBM PC compatible  
 \* OPERATING SYSTEM: PC-DOS/MS-DOS  
 \* SOFTWARE: PatentIn Release #1.0, Version #1.30  
 \* CURRENT APPLICATION DATA:  
 \* APPLICATION NUMBER: US/08/511,485  
 \* FILING DATE: 04-AUG-1995  
 \* CLASSIFICATION: 514  
 \* ATTORNEY/AGENT INFORMATION:  
 \* NAME: Clark, Paul T.  
 \* REGISTRATION NUMBER: 30,162  
 \* REFERENCE/DOCKET NUMBER: 07540/002001  
 \* TELECOMMUNICATION INFORMATION:  
 \* TELEPHONE: 617/542-8906  
 \* TELEFAX: 617/542-8906  
 \* TELEX: 200154  
 \* INFORMATION FOR SEQ ID NO: 8:  
 \* SEQUENCE CHARACTERISTICS:  
 \* LENGTH: 618 amino acids  
 \* TYPE: amino acid

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; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-8

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Query Match	6.38;	Score 462;	DB 2;	Length 618;
Best Local Similarity	24.78;	Pred. NO. 2.1e-33;		
Matches 159;	Conservative 93;	Mismatches 238;	Indels 154;	Gaps 24;

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0Y 38 LEEEOGRAMOGGYNSOMSEAKRLKTFVTPYPSWMP---QEWAAAGPFTGKSG 94
Db 28 L$DWTNSKKOKMKD$FSE-----LYRMSTYSTFAGVPSYRSRLARGAFYTGVDK 80
0Y 95 IOCFCCSLILFAGLTRLPJEDHNRFPDPCF---LTKDVGNIATYDIPVKN----- 144
Db 81 VKCFCCGLMDNMWKLGDSP10KHQOLPSCFSCFIONLVASISGTSKMTSPMRNSFALS 140
0Y 145 -----LKSRL-----RGGKRY--QEEBALASFRMPPFYOG 175
Db 141 PTLHSSLFSGSYS$LPNPPLNS$AVEDISSRNPYSYAM$TEEARFLYHMP--LTF 198
0Y 176 ISPCVLEAGVFVTGKODTYOFC$GCGGLQNMEEGDDPMKHA$WPKCFEFLSKSGSEE 235
Db 199 LSPSLAAGYTYIGPGRVAC$PACGGL$MWEKDDAMSEHRH$FNCFPL---ENSLE 255
0Y 236 ITQYIOSYKGV$DITGEHFVNSWQRELPMASAYCND$IFAYEBRLDSEKDPRESAVG 295
Db 256 TLRFSIS-----NLSMQT-----HABRRTFMYP$SPVQ 286
0Y 296 VAALAKALFTYTGIKDIYOCF$GCGGLEKNOEGDDPLDHRCP$RPNP$LONNKSSAEVT 355
Db 287 PEOLASAFYTYVGRNDYKCCGCGGLGCMWSSGDDPWEHAKM$PREFLIRMGQ--EFV 34.5
0Y 356 PDLQSR-GELCELETTSESNI$ED$IV$P$VPM$AG$EAO$MFO$EAKNLEO$RAAT$A 414
Db 346 DEIQGRPHLEQLLST$DTG$EEN--ADP$IIHF$G$E$S--SEDAVAMMT$PVYK$ALEM 402
0Y 415 SF-----RHSULDI$SSL-----ATHLLGCDL$IAS 442
Db 403 G$NDLVKQTVL$KILTTGENYK$VND$IV$AL$LA$E$DEK$EKEK$EKOAE$M$ASD$SLIR 462
0Y 443 KHISK$P$V$P$V$L$VE$V$GNL---$N$V$C$VE$E$AG$G$TVL---L$K$IA$F$LA$SG--- 490
Db 463 KNBALRQQLCVLRPIDNLLK$AN$V$IK$Q$E$ND$IK$Q$T$YR$Q$ARE$LD$T$IVW$K$G$N$A$N 522
0Y 491 ----CCPLNRFQVLYLSIS$TR-----PD$EGL$AS$ITCQ$ULEK---EG$SV$TECM$RNI 539
Db 523 I$K$M$C---L$KEID$T$LVK$N$L$FVD$KNM$K$YIP$ED$V$G$S$L$E$EQL$RRL$Q$E$RT$K$C$MD$KEV 579
0Y 540 QOLKNOVFL$LD$V$K$EIS$IP$OY$G$K$LO$K$N$H$S$R$T$OLL$AV$RT 583
Db 560 ----$V$E$IF$G$H$L$V$C---Q$E$C$A$S$IR$K$P$C$IR$G$II$K$G$V$RT 615

```

RESULT 4  
US-09-212-971-8  
Sequence 8, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212.971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017.354

Tue Oct 1 09:27:20 2002

us-09-830-338-1.rail

EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-212-971-8

Query Match  
Best Local Similarity 24.7%; Score 462; DB 3; Length 618;  
Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;

38 LEEEOEKERAKKMGKGYNSOMRSEAKRLKTPVTEPYSWIP---QEMAAAGFTGWSG 94  
28 LSWMTNSKOKMKYDPSCE-----LYRMSTYTFPAGVPVSESLAAGFTYTGVDK 80  
95 IOCFCCSLILFAGLRLPIEDHKRFHPDCG---LLNKDVGNIATYDIRVN----- 144  
81 VKFCGCGMLDMKMGKDSPIOKHQLYPCSCFIONLYSASLSTSKNTSPMNSFAHLS 140  
145 -----LKSRL-----RGCKMRY---QEBARLASFRNMPFYVG 175  
141 PTEHSLFSGSYSLPPLNPLNSRAVEDISSRTNPIYANSTEARFLTYHMP--LTF 198  
176 ISPVLSAGFVFTGKODTVOCFSCGCGCKLEKWEQEDDPLDHTPCFPCFLONMKSSAEVT 286  
199 LSPSELARAGFTYIGDRAVACFACGGLSWMEKPKDDAMSEHRRHPNCPFL---ENSL 235  
236 ITQYIOSYGFVDITGEHFVNSWQRELPMASAYCNDISFAVELDLDFKMPRESAVG 295  
256 TLRFSSIS-----NLMSQT-----HAARMRTFMWPSVYVQ 286  
296 VALAKAGLFTYGIKDIYOCFSCGCGCKLEKWEQEDDPLDHTPCFPCFLONMKSSAEVT 286  
287 PQLASAGFTYIGDRAVACFACGGLSWMEKPKDDAMSEHRRHPNCPFL---ENSL 235  
356 PDLQSR--GEICELLETTSESNLDSIAVGPVPEMAQEAQWFOEAKNLNOLRAAYTSA 414  
346 DEIGGRPHLEOLSTSDTGEEN--ADPPIHFGRESS--SEDAVMNMTPVYKSALEM 402  
415 SF-----RHMSLIDISSPL-----ATDHLGCDLSTAS 442  
403 GFRBDLVKOTVSKILTTGENTKYVNDIVSALLNAEDEKREKEKQAEEMASDLSLR 462  
443 KHTSKPVOEPLVLPVFCNL--NSVACVEGAGSGKTVL--LKTAFIWMASG----- 490  
463 KRMALFOQLICVLPILDNLKANVINKEHDIKOKTOPIQARELIDITWVGMAAN 522  
491 -----CCPLNFOVLPYLSLSTR-----PDGLASIIICDOLLEK--EGSVTECMNII 539  
533 IFKNC-----LKEIDSTLVKKNLFVDYKMKYIFTEVDYSGLSLEOLRLRLOEERTCVCNDKEY 579  
540 OQLNOVLFLDLDYKEICSIPOVIGKLTOKNHLSTCLLAVRT 583  
580 -----SVFTPCGHLVVC---QECAPSLKCPICIGIKIGKTVRT 615

RESULT 5  
US-08-800-929A-8  
Sequence 8, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneiluk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Layton, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-8

Query Match  
Best Local Similarity 6.3%; Score 462; DB 4; Length 618;  
Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;

38 LEEEOEKERAKKMGKGYNSOMRSEAKRLKTPVTEPYSWIP---QEMAAAGFTGWSG 94  
28 LSWMTNSKOKMKYDPSCE-----LYRMSTYTFPAGVPVSESLAAGFTYTGVDK 80  
95 IOCFCCSLILFAGLRLPIEDHKRFHPDCG---LLNKDVGNIATYDIRVN----- 144  
81 VKFCGCGMLDMKMGKDSPIOKHQLYPCSCFIONLYSASLSTSKNTSPMNSFAHLS 140  
145 -----LKSRL-----RGCKMRY---QEBARLASFRNMPFYVG 175  
141 PTEHSLFSGSYSLPPLNPLNSRAVEDISSRTNPIYANSTEARFLTYHMP--LTF 198  
176 ISPVLSAGFVFTGKODTVOCFSCGCGCKLEKWEQEDDPLDHTPCFPCFLONMKSSAEVT 286  
199 LSPSELARAGFTYIGDRAVACFACGGLSWMEKPKDDAMSEHRRHPNCPFL---ENSL 235  
236 ITQYIOSYGFVDITGEHFVNSWQRELPMASAYCNDISFAVELDLDFKMPRESAVG 295  
256 TLRFSSIS-----NLMSQT-----HAARMRTFMWPSVYVQ 286  
296 VALAKAGLFTYGIKDIYOCFSCGCGCKLEKWEQEDDPLDHTPCFPCFLONMKSSAEVT 286  
287 PQLASAGFTYIGDRAVACFACGGLSWMEKPKDDAMSEHRRHPNCPFL---ENSL 235  
356 PDLQSR--GEICELLETTSESNLDSIAVGPVPEMAQEAQWFOEAKNLNOLRAAYTSA 414



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Db 346 DEIGRYPHLEQLSTSDTGEEN--ADPPIHFGPESS--SEDAVAMNTPPVKSALEM 402
Oy 415 SF-----RHMSLIDISDL-----ANDHLGCDLSTAS 442
Db 403 GFNRDLVKQVILSKILTTGGENYKTVNDIVSALNAEDEKREKEKQAEEMASDLSLIR 462
Oy 443 KHISKVPOEPLVLEVEGNL---NSVMCEGEAGSGKTVL---LKKIAPLWASG----- 490
Db 463 KNRNALFQQLTCLPILDLNLKANYIKQEHDIKQKQIPLQARELIDITWKGNAAN 522
Oy 491 ---CCPLNRFQVLVFLYSLSSTR---PDEGLASIIDOLLEK---EGSYTEMCMRNI 539
Db 523 IFKNC---LKEIDSTLYKNLEFVDKNMKYIPTEDEYSGLSLEQLRLQGEERCKYCMDEY 579
Oy 540 QOLKNQVFLLDYKEICSIPOVIGKLIQKNHLSRTCLLIART 583
Db 580 ---SVFIFPCGHLVVC---QECAPSLRKCPCIGKIGITVRT 615

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# RESULT 6

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US-08-569-749-2
; Sequence 2, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569, 749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)396-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-749-2

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Query Match 6.3%; Score 462; DB 4; Length 618;  
 Best Local Similarity 26.0%; Pred. No. 2.1e-33;  
 Matches 155; Conservative 82; Mismatches 214; Indels 146; Gaps 22;

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Oy 38 LEEEOKERRAKKQKGNOMRSEAKRLKTFVYEPYSSMIP---OEMAAGFYFTGVKSG 94
Db 28 LSWDTNSKOKKKYFSCSE-----LYRMSTYTFPPAGVPSESLRAGGYTYGVNDK 80
Oy 95 IOCFCCSILFLGAGLTRLPIDEDKRFHPDCGF---LANKDVGNIAKYDIRVN----- 144
Db 81 VKCFCCGMLMDWMLGDSPIQKHQOLYPSCSPIQLVVASLGSSTSKNTSPMKNSPAHSLS 140

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Oy 145 -----LKSRL-----RGKARY---QEEPARLASPRNPFYVQ 175
Db 141 PTLHESSLFSGSYSLSPNPLNSRAVEDISSRTNPSTYAMSTEARLTTHMP--LTF 198
Oy 176 ISPCVLEAGEVFTGKQDTVOCFCSCGCLGNWEEGDDPMKEHAKWPCFELRSKSSSE 235
Db 199 LSPSELARAGFYTYIGRGVRACFACGKLSNWEPRDAMSHRRFRFPCPL---ENSL 255
Oy 236 ITQYIQSYKGFVDITGEHFVNSWQRELPMASAVCNSIFAYEELRLDSFKOMPRESAVG 295
Db 256 TLFESIS-----NLSMOT-----HAARMRTFMYWPSVYVQ 286
Oy 296 VAAALAKALFTYGIKDIYQCCSCGCLLEKNQEGDPLDDHTRCPNCFLOMKNSSAATV 355
Db 287 PEOLASAFYVYVGRNDVYCCDCDGLRCWESGDDPVWEHAKWPCFELLRMGQ--EFV 345
Oy 356 PDLQSR--GELCELLETTESNLEDIAVPIVPEMAQEAQFOEAKMLNEQLRAAYTSA 414
Db 346 DEIGRYPHLEQLSTSDTGEEN--ADPPIHFGPESS--SEDAVAMNTPPVKSALEM 402
Oy 415 SFRHMSLIDISSDLATDHLGCDLSIASKHISKVQEP-LVLEPEYGNLSVMCEGEAG 473
Db 403 GFNR-----DL-----VKQTVOSKILTTGGENYKTVNDIVSALLNAE 438
Oy 474 SGKTVLLK-KIAFLWASGCCPLNRFQVLVFLYSLSSTRPDEGLASIIDOLEKGSYTE 532
Db 439 DEKREEREKQAEEMASDLSLIRKNMALFQQLTCVLP-----LIDNLLK----- 484
Oy 533 MCMRNIIOQLKNQVFLLDYKEICSIPOVIGKLIQKNHLSRTCLLIARTNRARDI 589
Db 485 ---ANVIKQEHDI-----KQKQIPLQARELID-----TIVKQNAANI 523

```

# RESULT 7

```

US-09-617-053A-8
; Sequence 8, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617, 053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800, 929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-617-053A-8

```

Query Match 6.3%; Score 462; DB 4; Length 618;  
 Best Local Similarity 24.7%; Pred. No. 2.1e-33;  
 Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;

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Oy 38 LEEEOKERRAKKQKGNOMRSEAKRLKTFVYEPYSSMIP---OEMAAGFYFTGVKSG 94
Db 28 LSWDTNSKOKKKYFSCSE-----LYRMSTYTFPPAGVPSESLRAGGYTYGVNDK 80
Oy 95 IOCFCCSILFLGAGLTRLPIDEDKRFHPDCGF---LANKDVGNIAKYDIRVN----- 144
Db 81 VKCFCCGMLMDWMLGDSPIQKHQOLYPSCSPIQLVVASLGSSTSKNTSPMKNSPAHSLS 140

```

```

OY 145 -----LKSRL-----RGCKMRY--QEEEARLASFRMPPYVQG 175
DB 141 PTLHSLSESGSYSLSPNPLNSRAVEDISSRTNPNYSYAMSTEARFLTYHMP--LTF 198
OY 176 ISPCVLEAGFPFTGKOTVOCFSCGCGCLGMEGGDDPMKPKCEFLRSKSSSE 235
DB 199 LSPSLANAGFYIYIGPGRVACFACGCKLSNMEPKDAMSEHRHPNCPFL--ENSL 255
OY 236 ITOYIOSYKGFVDITGEHFVNSWVORELPMAAYCNDISFAYEELRDSFKDMPRESAVG 295
DB 256 TLRFSTIS-----NLSMOT-----HAARMRTFMWPSVVPYQ 286
OY 296 VAALAKAGLFYTGIDYVOCFSCGCGCLEKMEGGDDPLDHTRCFPCFLOMMSAEVT 355
DB 287 PEOLASAGFYVGRNDVYKFCGCGDGLRCWESGDDPMVHAKEWPFRCFLIRMGQ--EFV 345
OY 356 PDLOS-R-GEICELLETSSNLEDSIAVGPVPEMAOGEAOWFOEAKNLNQLRAAYTSA 414
DB 346 DEIGRYPHLEQLSTSDTTEEN--ADPPIIHGPRESS--SEDAVMNTPPVKSALEM 402
OY 415 SFRMSLIDISSDLATDHLGCDLSIAKHSKPYOEP-LVLPVEFONLSVMKVEGAG 473
DB 403 GFNRDLVKOTVLSKILTTGENTKYNDIVSALNAEDEKREERKEQAEMASDLSLR 462
OY 443 KHISKPYOEPVLPVEFONL--NSVMKVEGAGSCKTVL--LAKIAFLMAGS----- 490
DB 463 KNRMALFOQLTCVLPILDNLKNVINKOEHDIIKOKTOPLQARLIDITIVKGNMAAN 522
OY 491 -----CCLPLNFOQLVFLSLSTR-----PDEGLASIIDQLLER--EGSVTEMCKMRNI 539
DB 523 IFKMC---LKEIDSTLYKLNLFVDKNMKIYFTEDEVSGLSLEQLRLQEBRCKCMCKMEV 579
OY 540 QOLKNQVFLFLDDYKEICSIPOVYIGKLIQKNHLSTRCLLIIVTNRARDI 589
DB 580 -----SVFIFPCGHLYVC---DECAPSLRKCPCICGIIKGYVRT 615

RESULT 8
US-09-069-023-29
: Sequence 29, Application US/09069023A
: Patent No. 6348573
: GENERAL INFORMATION:
: APPLICANT: Nunez, Gabriel
: APPLICANT: Inohara, Naohiro
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
: FILE REFERENCE: US-03333
: CURRENT APPLICATION NUMBER: US/09/069,023A
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 29
: LENGTH: 618
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-069-023-29

```

Query Match 6.3%, Score 462, DB 4, Length 618;  
Best Local Similarity 26.0%, Pct. No. 2, 1e-33;  
Matches 155; Conservative 82; Mismatches 214; Indels 146; Gaps 22;

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OY 38 LEEEDQKERAKKOKYNSOMSEAKRLKTEVYEPYSWIP--QMAAGFYTGVSNG 94
DB 28 LSDWYNSKQMKKYDFSC-----LYRMSTYSTRPAGVPSERSLARAGFYTYGVNDK 80
OY 95 IQCFCCSLILFAGLITRPIEDHKRHPDCGF--LNRDVGNIAKYDVRVN----- 144
DB 81 VKFCGCGMLDMNWKLGSPISQKHQKQLPSCSFIONLYVASLSTSKNSPMRNSAHSLS 140
OY 145 -----LKSRL-----RGCKMRY--QEEEARLASFRMPPYVQG 175

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DB 141 PTLHSLSESGSYSLSPNPLNSRAVEDISSRTNPNYSYAMSTEARFLTYHMP--LTF 198
OY 176 ISPCVLEAGFPFTGKOTVOCFSCGCGCLGMEGGDDPMKPKCEFLRSKSSSE 235
DB 199 LSPSLANAGFYIYIGPGRVACFACGCKLSNMEPKDAMSEHRHPNCPFL--ENSL 255
OY 236 ITOYIOSYKGFVDITGEHFVNSWVORELPMAAYCNDISFAYEELRDSFKDMPRESAVG 295
DB 256 TLRFSTIS-----NLSMOT-----HAARMRTFMWPSVVPYQ 286
OY 296 VAALAKAGLFYTGIDYVOCFSCGCGCLEKMEGGDDPLDHTRCFPCFLOMMSAEVT 355
DB 287 PEOLASAGFYVGRNDVYKFCGCGDGLRCWESGDDPMVHAKEWPFRCFLIRMGQ--EFV 345
OY 356 PDLOS-R-GEICELLETSSNLEDSIAVGPVPEMAOGEAOWFOEAKNLNQLRAAYTSA 414
DB 346 DEIGRYPHLEQLSTSDTTEEN--ADPPIIHGPRESS--SEDAVMNTPPVKSALEM 402
OY 415 SFRMSLIDISSDLATDHLGCDLSIAKHSKPYOEP-LVLPVEFONLSVMKVEGAG 473
DB 403 GFNR-----DL-----VKOTVOSKILTTGENTKYNDIVSALINAE 438
OY 474 SGRTVLK-KIAFLMAGCCPLNFOQLVFLSLSTRPDEGLASIIDQLLEKSSVTE 532
DB 439 DEKREERKEQAEMASDLSLRNRMALFOQLTCVLP-----LIDNLK----- 484
OY 533 MCMRNIOQLKNQVFLFLDDYKEICSIPOVYIGKLIQKNHLSTRCLLIIVTNRARDI 589
DB 485 -----ANVINKOEHDIT-----KOKTOPLQARLID-----TIVKGNMAANI 523

```

```

RESULT 9
PCT-US96-12860-2
: Sequence 2, Application PC/TUS9612860
: GENERAL INFORMATION:
: APPLICANT: TULARIK, INC.
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESSES:
: ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/12860
: FILING DATE: 06 AUG 1996
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Brezner, David J.
: REGISTRATION NUMBER: 24,774
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)781-1989
: TELEFAX: (415)398-3249
: INFORMATION FOR SEQ ID NO: 2:
: LENGTH: 618 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US96-12860-2

```



## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Pastes for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,929A

FILING DATE: 13-FEB-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,590

FILING DATE: 14-NOV-1996

APPLICATION NUMBER: 60/017,354

FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bleker-Brady, Kristina

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 07891/009001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 612 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800-929A-14

## Query Match

Best Local Similarity 26.68; Score 457.5; DB 4; Length 612;

Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

QY 43 OKERAKMKG---YNSOMRSEAK-----RLKTFVTEPYSSMTP---OEMAAGFYFT 89

DB 16 OKLRIMKSTILSNMTKESEKMFDFSCGLYRMSTYSAPFRGVSEERSLARAGFYTT 75

QY 90 GYKSGIOCFCSLILFGAGLRLPIEDHKRFRHPCDGF---LANKDVGNLAKYDIRKNLK 146

DB 76 GVDNKKVCCGGLMDNMKGDSPEVKHROFYPCSFVOTLLSASLOSPSK---NMSPVK 132

QY 147 SRL-----RGG-----KMYOEERLARSFRMPPYVQ 174

DB 133 SRFHSSPFLERGGIHSNLCSPLNSRAVEDFSSRMDCSTAMSTEERARLTYSMP--LS 190

QY 175 GISPCVLSAEGFVFTGKODTVOCFSCGCGCLGNWEGDDPKWEHAKWPKCEFLRSKSS 234

DB 191 FLSPAEIARAGFYIIGPDVACFACCGKLSMWERPKDAMSEHRRHFPHPCEFLRMSGO-EF 250

QY 235 EITQYIQSYKGFVDITGHEHFNVSWMQRELPMASAYCNDISFAVEELRLDSFKDMPRESAV 294

DB 251 RFS-----ISNLSMOTHSARLRTFLYMPSPVPV 278

QY 295 GVAALAKAGLFYTGINDIVOCFSCGCGCLEKMOEGDDPLDDHTRCFPPVCPFLONKSSAEV 354

DB 279 QPQLASAGFYIYVDRNDVACFCDCGGLRCWEPGDDPWIEHAKWPKCEFLRMSGO-EF 337

QY 355 TPDLOS-R-CELCLEETSESUNLEDSIAGVPIVEMAQGEAOWFOEAKNLEQLRAAYTS 413

DB 338 VDEIQARVPHLEQLSTSDTPGEBNADPTETVYHFGPGE-----SS 379

QY 414 ASFRHMSLLDISDLADHLLGCDLSIASKHISKPYOEPVLYRVEVGNUNSVWCV---E 469

DB 360 KDVMMSPPVYKALE---NGFSRLVROTVOQT---LATCENTRIVINDIVSLNAE 432

QY 470 GEAGSGKTVLLKTAFLMASGCGPLNRLQVLYVYLSLSTRPDEGLASIIQOLLEKSGS 529

DB 433 DERREEK---ERQTEPMASGDSLIRKNRMALFOQLTHVLP-----LIDNLL--EAS 480

QY 530 VTECHMNIIOQLKNQV 546

DB 481 VITKQEHDIRO-KTQI 496

## RESULT 12

US-08-569-749-14

Sequence 14, Application US/08569749

Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)398-3249

TELEFAX: (415)781-1989

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 612 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-749-14

## Query Match

Best Local Similarity 26.68; Score 457.5; DB 4; Length 612;

Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

QY 43 OKERAKMKG---YNSOMRSEAK-----RLKTFVTEPYSSMTP---OEMAAGFYFT 89

DB 16 OKLRIMKSTILSNMTKESEKMFDFSCGLYRMSTYSAPFRGVSEERSLARAGFYTT 75

QY 90 GYKSGIOCFCSLILFGAGLRLPIEDHKRFRHPCDGF---LANKDVGNLAKYDIRKNLK 146

DB 76 GVDNKKVCCGGLMDNMKGDSPEVKHROFYPCSFVOTLLSASLOSPSK---NMSPVK 132

QY 147 SRL-----RGG-----KMYOEERLARSFRMPPYVQ 174

DB 133 SRFHSSPFLERGGIHSNLCSPLNSRAVEDFSSRMDCSTAMSTEERARLTYSMP--LS 190

QY 175 GISPCVLSAEGFVFTGKODTVOCFSCGCGCLGNWEGDDPKWEHAKWPKCEFLRSKSS 234

DB 191 FLSPAEIARAGFYIIGPDVACFACCGKLSMWERPKDAMSEHRRHFPHPCEFLRMSGO-EF 250

QY 235 EITQYIQSYKGFVDITGHEHFNVSWMQRELPMASAYCNDISFAVEELRLDSFKDMPRESAV 294

DB 251 RFS-----ISNLSMOTHSARLRTFLYMPSPVPV 278

QY 295 GVAALAKAGLFYTGINDIVOCFSCGCGCLEKMOEGDDPLDDHTRCFPPVCPFLONKSSAEV 354

DB 279 QPQLASAGFYIYVDRNDVACFCDCGGLRCWEPGDDPWIEHAKWPKCEFLRMSGO-EF 337



```

Qy 147 SRL-----RG-----KRYOEERARLAFRANPFYVO 174
Db 133 SRFAHSSPLERGGIHSNLCSSPLANSRAVEDFSSRMDPCSYAMSTEARLFTYSMP--LS 190
Qy 175 GISCVSEAGFVFTGKODTVOCFSCGCGCLGNWEGDDPKREHAKWPCFELRSKSSSE 234
Db 191 FLSPAEIARAGFYTIGPGRVACFACGKLSNWEPRKDAEMSRHRHFCFPLETSETQ 250
Qy 235 EITQYQSYKGFVDITGEHFVNSWQRELPMASACNCSITAYELRLDSKDPRESAV 294
Db 251 RFS-----ISLNSQTSARLRTFLYPPSPV 278
Qy 295 GVALAKAGLFTYGIKIDVOCFSCGCGCLEKQOEGDDPLDHTRCFPNCPFLONKSSAEV 354
Db 279 OPEQLASAGFYTVDRNDVKCFCCDGLRCWEPGDDPWVEHAKWPCFELRLNKGQ-EP 337
Qy 355 TPDLDSR-GEICELLETTSESNEISIAVGPVPMAGQEMFOEAKNLNEQLRAAYS 413
Db 338 VDEIQAARYPHLEQLLSTSDTPGEMNDPTEYVHFGPGE-----SS 379
Qy 414 ASFRHMSLIDISDLATDHLGCDLSIASKHSKPVQEPVLPEVFGNLSVMCV-----E 469
Db 380 EDVYMSRTPVYKALE---MGFSRLVQTVOROI---LATGENTRYNDIVSVLLNRE 432
Qy 470 GEAGSGKTVLKIATFAMASCCPLNRFOLVFLYLSSTRDEGLASTICCOLLEKESG 529
Db 433 DERREER---ERQTEEMASGDLILIRKNMALFOQLTHVP-----ILDNL--BAS 480
Qy 530 VTECMNRNIIOQLKNOV 546
Db 481 VITKQEHDIIRQ-KTOI 496

RESULT 15
US-09-212-971-12
; Sequence 12, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; EARLIER FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-212-971-12

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Query Match  
Best Local Similarity 6.0%; Score 440; DB 3; Length 600;  
Matches 145; Conservative 88; Mismatches 226; Indels 162; Gaps 19;

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Qy 47 AKMKGYS-----QMRSEAKRLTFVITYEYSWIP---QEMAAAGFYFTGVKSGIOCF 98
Db 9 AKIMKSAVTFELKDFSCGLYRLS---TYSAPRGVPSVRSERSLARAGFYTYTGANDKVKCF 65

```

```

Qy 99 CSSLIFGAGLRLRIEDHKKRPHDCGFLNKDVGNIKAYDIRVKNLSRLRGKMY-- 156
Db 66 CCGMLDNNKQODSPMEKRRKLYPCSNFVOTLNPANSLEASPRSLSTANSTMPUSFAS 125
Qy 157 -----QEEARLASFRNMPFYVGIS 177
Db 126 SENTGFSGSYSSFPSPDVNFRANDOPALSTSPYHFAAMTEARLLTYETWP--LSFLS 183
Qy 178 PCVLSAGFVFTGKODTVOCFSCGCGCLGNWEGDDPKREHAKWPCFELRSKSSSEIT 237
Db 184 PAKLAKAGFYITIGDGRACACDGLRCWESGDDPWVEHAKWPCFELRLNKGQFYSO 239
Qy 238 QYISYKGFVDITGEHFVNSWQRELPMASAYCNDST-FAYEELRLDSKDPRESAVG 296
Db 240 -----ASRYVSNLSQTHAARIRTFSSNPPSSALVHS 271
Qy 297 AALAKAGLFTYGIKIDVOCFSCGCGCLEKQOEGDDPLDHTRCFPNCPFLONKSSAEVTP 356
Db 272 QELASAGFYTTGHSDDVKCFCCDGLRCWESGDDPWVEHAKWPCFELRLNKGQFYSO 331
Qy 357 DIOSRGELCELLETTSESNEISIAVGPV-----PMAGQEMFOEA 400
Db 332 VOAGYPHLEQLLSTSDSP-EDENADAAIVHGPESSEDDVYAMSTPVYKALEMGFSRS 390
Qy 401 ---KNLEQLRAA---YTSASFRHMSLIDISDL-----ATHLLGCDLSIASKHSK 447
Db 391 LVROTVQROILATGENYRTVSDVLIGLDABDEMREQEMQAAEEESDDIALIRKNKY 450
Qy 448 PVOE-PLYLPEVFGNLSVMCVGEAGSGKTVLKIATFAMASCCPLNRFOLVFLYLSL 506
Db 451 LFOHLTCVPMPLVCLLSARAITEQECNAV----- 480
Qy 507 SSTRPDEGLASTICDOLLEKESVTECMNRNIIOQLKNOV---LFLLDYK-----EICS 558
Db 481 --QKPHTLQASTLIDTVLAK-GNNAATSPRNSLKEIDPALYRIDIFVQODIRSLPTDIA 537
Qy 559 IP--OVICKLLOKHNLSYTC 577
Db 538 LPMEQLRLK-QEBRMCKVCM 557

```

Search completed: September 30, 2002, 15:04:59  
Job time: 245 sec